Human T139 protein DNA encoding novel DNA encoding novel Human ovarian carc Ovarian carcinoma Human Protease and

AAS76343 AAA70010 ABN72904

DNA encoding novel Human sbg1002620TI Human sbg1002620TI Human LP095 secret Rat EST-derived co Human protease-inh

AAS73137 ABL57727 ABL57728

AAD38692

1210 1789 1206

AAS81 AAS9.

AAF77686 AAD17765

AAH15690

ABK33563

Human CDNA clone r DNA encoding novel DNA encoding novel DNA encoding novel

AAK93233 AAS76345 AAS88505 AAS89242 AAS88505 AAS89242 AAS81207

DNA encoding novel Human EST-derived Human cDNA 5'-end

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PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA clone encoding human PRO347, amplified in tumour cells.
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201..1487
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       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Result 2

cancer agent novel trypsi cDNA clone (

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                                                                                                                                                                                                                                  This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532) coding for human PRO347 (UNQ306) (see AAV06482). The clone was isolated from a foetal kidney library. Amplification of DNA44176 occurs in various tumours, suggesting an association with tunmour formation or growth. Antagonists (e.g. antibodies) directed against PRO347 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                               Antibody against proteins expressed in neoplastic cells, useful
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98US-0088742.
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Matches 1876; Conservative
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P-PSDB; AAY06483.
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transmembrane proteins used therapeutically. The PRO proteins have extrostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy identification of homologues, raising antibodies and design of probes
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                   1801 TGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAATCAG 1860
                                                                                                                                                                                                                                                                                                                         Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder; ss.
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and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
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                                   PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                           Lawrence DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                        Gurney AL, Hillan K,
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell growth and proliferation -
             cDNA encoding novel polypeptide PRO347.
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 50; Fig 13; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and proliferation in mammals.
                                                                                                                                                                                                                                                                                                 99WO-US21090.
99WO-US28313.
99WO-US28409.
                                                                                                                                                                                                                                                                         99WO-US12252
99WO-US20111
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99WO-US28565
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Matches 1876; Conservative
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                                                                                                                                                                    WO200037640-A2
                                                                                           Homo sapiens.
                                                                                                                                                                                                                                              22-DEC-1998;
08-MAR-1999;
02-JUN-1999;
01-SEP-1999;
15-SEP-1999;
                                                                                                                                                                                                                                                                                                              30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                     Botstein D,
                                                                                                                                                                                              29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplastic
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qq	181	TCCTTGGCACCACCTGGGCAGAGGTGTGGGCCACCCCAGCTGCAGGAGCAGCTCCGATGG 240
٥y	241	CGGAGCCCTGAACAGGAAGAGTTTCTTGCTCCTCTCCCTGCACACACCGCCTGCGA 30
Op	241	SAGCCCTGAACAGGAAGGAGATTCTTGCTCCTCTCCTGCACAACGGCCTGCGCA 30
Qy Db	301	GCTGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCC 360
Qy	61	AACTGGCTCAAGCCAGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCGGGCC 420
QD .	19	SIGNICANGCICAGGCACTCICICIGGAAAITCCCAAACCCGGGGCCTGGCATCCGGGCCCTAACCCGGGCCCTGGGGGCGCCTGGGGGCGCCTGGGGGGCGCGGGGGG
Oy Dp	421	0 00
ΛO	481	TTGAAGTGGTCAGCCTATGGT
qq	00	
QY Db	541	AGTGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCC 600
ΟŸ	601	AGCTGGGCTGTGGGCGCACTGTGCTCTGCAGGCAAAACGAAAGCCTTTGTCT 660
Dp	601	engegererenge de la contraction de la contractio
δy	661	Ñ
qq	661	CTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGA 72
Oy odd	721	AGGGTGCCTGGTGTTCGCTCTGCACACGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC 780
Qy	∞ `	4
Dp	781	GGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG 84
QY	841	GACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGGATACT 900
ΟŊ	901	GCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
qq	901	######################################
Qy Dp	961	GCGTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTCCCTTCC 1020
Qy	1021	ACACCTGTGACCAGGGACGACGGAGGCTGCTTCATGGTGTCTTCAGAGGCAGACACCT 1080
qq	1021	TGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACC
۲٥ م	80	ATTACAGAGCCAGGATGAATGTCAGAGGAAGGCGGGTGCTGGCCCAGATCAAGAGCC 1140
Op	30	ATTACAGAGCCAGGATGAAATGTCA6AAGGAAAGGGGGGGGGG
Qy Db	1141	AGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAAGGGTGA 1200
δλ	1201	. CTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGCTCACCACAAAAACGCGCCAAGG 1260
g ;	1001	16ACA61106ACA11CGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
O.Y D.D	1261	ACTCCTTCCGCTGGGCCACAGGGGGGCCAGGCCTTCACCAGTTTTGCCTTTGGGCCAGGCTTCACCAGGCCTTCACCAGGCCAGGCCAGGCCAGGCCTTCACCAGTTTTGCCTTTGGGCAGC

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1681 AGAAGAAGCTGGGGCCCTTCGCCTGCTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740
                                                                     1561 GGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 1620
                                                                                                                                                      1681 AGAAGAAGCTGGGGGCCCTTCGCCTTTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740
                                   1381 IGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACA 1440
                                            1321 CIGACAACCACGGGCIGGIGIGGCIGAGIGCIGCCAIGGGGIIITGGCAACIGCGIGGAGC 1380
          PRO; membrane bound protein; secreted protein; PRO357; PRO343; PRO15; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= PRO347 polypeptide
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123..1490
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98US-0112850.
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16-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described. The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAACAAGCCGGGTGGCTGAGCCTGTGCACGGAGCACCTGACGGGCCCCAACAGAC 120
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                                                                                                                                              Godowski PJ, Grimaldi CJ, Gurney AL;
Apler MA, Roy MA, Tumas D, Wood WI;
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                                                                                                                                                                      Napier MA,
                                                                                                                       Eaton DL,
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Matches 1876; Conservative
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                                                                                                                 Botstein D,
                                                        (GETH ) GENENTECH INC
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                                                                                                                                     Gerritsen ME,
  22-DEC-1998;
                                                                                                                                                                   Hillan KJ,
                                                                                                                 Baker KP,
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             AGCTGGGCTGTGGCGCCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCT
                                                 AGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC
                                                                                                                                781 ATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG
                                                                                                                                                                                GACGICICAACAICAGCACCIGCCACIGCCACIGICCCCCIGGCIACACGGGCAGAIACI
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us-09-944-896-49.rng

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1084 ACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAGA 1143
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                        124 IGCIGCAICCAGAGACCICCCCIGGCCGGGGGCAICICCIGGCIGIGCICCIGGCCCICC 183
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                                                                                                             141 IGCIGCATCCAGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCTCC
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64 AACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 26 human secreted polypeptides, useful e.g. for preventing, diagnosing and/or treating cancers and for promoting wound
                                                                                                                                                    TGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAAATTATGAATCAG 1860
                                                                                                                                                                            1681 AGAAGAAGCTGGGGCCCTTCGCCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, pyraft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and any involving abnormal anglogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 94.7%; Score 1776.2; DB 22; Length 1923; Best Local Similarity 97.8%; Pred. No. 0; Matches 1832; Conservative 0; Mismatches 13; Indels 28; Conservative 0; Mismatches 13; Mism
                                                            1741 GAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCC
                                                                                     The present invention relates to 26 secreted human proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1923 BP; 444 A; 568 C; 569 G; 342 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 416-417; 530pp; English.
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AAF24152
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1204 ACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGACT 1263
                                       CCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCTG 1323
                                                                                                       ACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTGC 1383
                                                                                                                     1384 AGGCTICAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACATCT 1443
                                                                                                                                                        GCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACAT 1503
                                                                                                                                                                                              GGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGA 1563
                                                                                                                                                                                                                                  ACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAAT 1623
                                                                                                                                                                                                                                                                        AGAAGCIGGGGCCCTICGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAA 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; T139 polypeptide; immune system disorder; spermatogenesis; ss; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                       1804 GGGGCAGCGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAATCAGCTG 1863
                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "T139 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ23299 standard; cDNA; 1856 BP
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This cDNA encodes a human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 cDNA insert is deposited with ATCC under accession number 98604. The T139 polypeptides and polynucleotides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant T139 expression or activity. especially proliferative or differentiative disorders, e.g. of the immune system. They can be used to modulate spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat disorders related to defects in sperm-egg fusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively binding compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating polypeptide activity. The polynucleotides are useful for producing probes or primers that selecting the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant tisk for or having a disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate to provent T139 expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 GCTCCATCCAGCCTGAGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 ACGGGCCCAACAGACCCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGGCATCTCCTGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 CTGTGCTCCTGGCCCTCCTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 AGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCCTGC 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 27; Gaps
                                                                                                                                                                                                                                                           Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.3%; Score 1751; DB 20; Length 1856; 98.0%; Pred. No. 0;
11ve 0; Mismatches 10; Indels 27;
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                                                                                                                               (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 1; 115pp; English.
                                                          96880SD-0M66
                                                                                            98US-0065661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.0%
Matches 1794; Conservative
                                                                                                                                                                                                      WPI; 1999-633969/54.
                                                                                                                                                                                                                         P-PSDB; AAY41266.
                                                      23-APR-1999;
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                                                                                                                                                                    Holtzman D;
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1306 TIGCCTITIGGGCAGCCTGACAACCACGGGCTGGTGGCTGAGTGCTGCCATGGGGTTTG 1365
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1098 CCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGA
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                                                                                                                                                                                                                                                                                   GCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGCCCACTGTCCCCCTGGCT
                                                                                                                                                         646 TAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAA
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                                                                                  586 GGGCCACCTCAAGCCAGCTGGGCGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGA
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                                                                        526 GCCACGCGGCAGGAGAGTGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGT
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Human; haematopoiesis; clotting; kidney failure; wound healing; cancer; neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease; heart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive; glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; heamostatic; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic; cytostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilliser; hypotensive; tumour; injury; trauma; antianginal; vasotropic; antiulcer; apoptotic disorder; rheumatoid arthritis; cardiant; renal disorder; rheumatoid arthritis; cardiant; renal disorder; T139; gene; ss.
                                                                                                                                                                                                                                    ACCTGGCCCAGACCCTGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCCACGGGGTAT 1845
                                                                                                           CTTCAATTAGATGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAAAGGCTGCTCTTTCC 1785
                                                                                                                                                                                                                                                                                               1731 ACCTGGCCCAGACCCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACAGGGTAT 1790
                             1546 TCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGG 1605
                                                                                           1606 TCTCAGACCTTGCACAATGCCAGAAGTTGGGCAGAAGAGGCAGGGAGGCCAGTGAGGC 1665
                                                                                                                                                         CAGGGAGTGAGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGTTTTGATTGGGAAGATGGG 1725
1431 CCTGAGGCCTGACCACATGGCTCCCTCGCCTGGGAGCACCGGCTCTGCTTACCTG 1490
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/note= "This region designated as SEQ.ID.NO.3 is
specifically referred in claim 27"
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95..1432
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/product= "Human T139 protein"
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95..1435
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Holtzman DA, Goodearl ADJ, Mccarthy SA;
98US-0065363,
98US-0065661.
98US-0102705.
98US-0124538.
                                                          99US-0298531.
                                                                        99US-0337930
                                                                                       99us-0363630
                                                                                                             (HOLT/) HOLTZMAN D A.
(GOOD/) GOODEARL A D J.
(MCCA/) MCCARTHY S A.
                                                                                                                                                                                                  WPI; 2002-303420/34.
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                                                                      22-JUN-1999;
                         22-JUN-1998;
 23-APR-1998;
             23-APR-1998;
                                          29-JUL-1998;
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Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders

Claim 26; Fig 1; 138pp; English.

The invention relates to nucleic acids encoding a variety of proteins burman T139 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-125), Muman T175 or murine WDNM-2, having diagnostic, preventive, to inhibit a proteinase activity, to modulate call-cell interactions, neamatopoiesis and the ability to modulate call-cell interactions, neamatopoiesis and the alinity to modulate call-cell interactions, neamatopoiesis and the annual to modulate call-cell interactions of the invention are useful for diagnosing and treating and treating and cartivity. The callular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful for treating kidney defects such as kidney fallure, carating cancer, are useful for treating neonet, TANGO-110 (TANGO-125) is useful for treating hound healing and for treating cancer, TANGO-110 (TANGO-125) is useful for treating hound healing and for treating cancer, TANGO-110 (TANGO-125) is useful for treating and for treating cancer, TANGO-110 (TANGO-125) is useful for treating modulating and for treating cancer, TANGO-110 (TANGO-125) is useful for treating modulating and for treating cancer, are useful to treat pancreatitis, creating and for treating modulations and tumours, and injury or trauma ischaemic heart disease, and tumours, and injury or traumal kidney) disorders, such as glomerular disorders, such as glomerular disorders, model and contracting proliferative disorders, such as glomerular disorders, acut and disorders, hyperplasia of the endometrium. TANGO-110 is useful for treat contracting proliferative disorders, inflammatory disorders, TANGO-175, or treating proliferative disorders, inflammatory disorders, religious erythematosus, inflammatory disorders, viral (Mondel apoptotic disorders, religioned apoptotic disorders, religioned and insorders, religioned in gene therapy. The present sequence is human T1139 cDNA.

Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;

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                                                              GCTCCATCCAGCCTGAGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTG 105
                                                                                                                           106 ACGGCCCAACAGCCCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGG 165
                                                                                                                                                                                         166 CTGTGCTCCTGGCCCTCCTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGG 225
                                                                                                                                                                                                          78 ACGGCCCAACAGACCCCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCCATCTCCTGG 137
                                      27; Gaps
                                                                               93.3%; Score 1751; DB 24; Length 1856;
                    Pred. No. 0;
0; Mismatches 10; Indels
                98.08;
           Best Local Similarity 98.0° Matches 1794; Conservative
Query Match
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AGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGAGTTTCTTGCTCCTCCCTGC
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                                                                                       GTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGA
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                      1278 INGCCITIGGGCAGCCTGACAACCAC-------GGGTTTG 1310
                                                         CCCGAAACCGTIACATCTGCCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGT 1485
1306 TIGCCTITGGGCAGCCTGACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTG 1365
                                             GCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAA 1425
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                                                                                                       Kawai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa T, Isogai T, Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                           Human full-length cDNA, SEQ ID NO: 2850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK94246 standard; cDNA; 1786
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02-MAY-2000; 2000JP-0183765.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length
                                                                                                                                                                                                                                                human cDNA of the invention.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in CD-ROM format directly from EPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCTGGCCCTCCTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAG 230
                                                                                                                                                                                                                                                                                                                                                                                                                        51 ATCCAGCCTGAGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830 Primers useful for synthesizing full length cDNA clones and their
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                                                                                                                                                                                                                                                                                                                                                   92.2%; Score 1729.8; DB 22; Length 1786; 97.8%; Pred. No. 0;
                                                    Claim 8; SEQ ID NO 2850; 1380pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                       Seguence 1786 BP; 361 A; 548 C; 553 G; 324 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                          use in genetic manipulation -
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Matches 1774; Conservative
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CAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACG 890
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                                                     GGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAG 950
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Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple scierosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive, antinifertility; antiniflammatory; ss.
                                                                                                                                                                                                                                                                                                                        /product= "Mature human protein with hydrophobic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins with hydrophobic domains and the nucleic acids encoding
                                                                                      Human protein having hydrophobic domain encoding cDNA clone HP10760.
                                                                                                                                                                                                                                                        /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
                                                                                                                                                                                                                         Location/Qualifiers
                     AAD12570 standard; cDNA; 1775 BP.
                                                                                                                                                                                                                                                                                                                                                                                                             2000JP-0000585.
2000JP-0000588.
2000JP-0002299.
2000JP-0026862.
2000JP-0058367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROT-) PROTEGENE INC.
(SAGA ) SAGAMI CHEM RES CENT.
                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2000; 2000WO-JP09359
                                                               25-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-418355/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kato S, Kimura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAE06575.
                                                                                                                                                                                                                                                                                                                                             WO200149728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-2000; 2
11-JAN-2000; 2
03-FEB-2000; 2
                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                   12-JUL-2001
                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                    mat_peptide
                                          AAD12570;
RESULT 9
         AAD12570
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The present sequence is human protein with hydrophobic domain encoding CDNA clone HP10760. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of

TATGAATCAGCTG 1863 = = = = = =

1851

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them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation

Claim 4; Page 271-275; 563pp; English.

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as multiple sclerosis,
  autoimmune disorders such
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microbial infections and autoimmune disorders such as multiple sclerosi- rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, luntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controllin fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth. Sequence 175 BP; 360 A; 541 C; 549 G; 325 T; 0 other; Query Match 91.7%; Score 1721; DB 22; Length 1775; Heast Local Similarity 97.9%; Pred No. 0; Mismatches 10; Indels 27; Gaps	63 AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCAC 2 AAACAAGCCGGGTGGCTGACCAGGCTGAGCCAGGCTGAGCAGCCGGGTGAGCGAGC	12	183 CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGTCCGATGGCC	243 GGAGCCTGAACAGGAAGAGTTTCTTGCTCCTCTCCTGCACAACCGCCTGCGCAGC	303 TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGACAGCCTGGCCCAA	363 CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTG	423 TGGGGACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTGGCGTCCTTT	483 GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGCAGCGGTACAGCCACGCGCAGAGAG 	543 T 482 T	y 603 CTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGT	y 663 GCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAG 	A 723 GGTGCCTGGTGTTCGCTCTGCACACCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT	QY 783 GCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA	QY 843 CGTCTCAACATCAGCACTGCCACTGCCACTGTCCCCTGGCTACACGGGCAGATACTGC Db 782 CGTCTCAACATCAGCACTGCCACTGCCACTGTCCCCTGGCTACACGGGCAGATACTGC	Oy 903 CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC
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1743 AGGAGAGGACACCGCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGACCTG 1802
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                                         AAS91790 standard; cDNA; 1934 BP.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving currentiating a polypeptide in tissue, as molecular weight markers and as fundating of sites expressing (II). (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity manno acid sequences. AAS64197-AAS94564 represent novel human cold diagnostic coding sequences of the invention.

Condensity of sequences of the invention.

Condensity of sequences of the invention.

Condensity of sequences of the invention of mutantions and the printed copies expensed to the printed in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CATGCTGCATCCAGAGACCTCCCCTGGCGGGGGGCATCTCCTGGCTGTGCTCCTGGCCCT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 CCTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGTCCGATGGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 45; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.2%; Score 1636; DB 23; Length 1934; 95.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1934 BP; 409 A; 577 C; 576 G; 372 T; 0 other;
                                        DNA encoding novel human diagnostic protein #27594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 27594; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
  13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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                                                                                                                                                                       WO200175067-A2.
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242 GGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCCCTGCACAACCGCCTGCGCAG 301
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Human; T139 polypeptide; immune system disorder; spermatogenesis; ss; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
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                                                                                                                                                                                             1603 AGGICICAGACCIIGCACAAIGCCAGAAGIIGGGCAGAGAGGAGGCAGGGAGGCCAGIGAG 1662
                                                                                                                                                                                                                                                                                               1663 GGCCAGGGAGTGAGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGAT 1722
                                                                                                                                                                                                                                                                                                                                                         1713 GGCCAGGGAGTGAGTGTTAAAAAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAAT 1772
                                                                                                                                                                                                                                                                                                                                                                                    1723 GGGCTTCAATTAGATGGCGAAGGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTT 1782
                                                                                                                                                                                                                                                                                                                                                                                                              1773 GGGCTTCAATTAGATGGCGAAGGAGGACCCCGCCAGTGGTCCAAAAAGGCTGTTTT 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                       1783 TCCACCTGGCCCAGACCCTGTGGGGCAGCGAGCTTCCC---TGTGGCATGAACCCCACG 1839
                                                                                                 AACTGCGTGGAGCTGCAGCTTCAGCTGCCTTCAACTGGAACAACCAGCGCTGCAAAACC 1472
                                                                                                                                                                              TCCTGAGGCCTGACCACATGGCTCCCTCGCCTGGGAGCACCGGCTCTGCTTACCT 1544
1320 AAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTT 1379
                                                                          1368 AACTGCGTGGAGCTGCAGGCTTCAGCTGCAACTGGAACGACCAGCGCTGCAAAACC 1427
                                                                                                                           CGAAACCGTTACATCTGCCAGGTTGCCCAGGAGCACA-TCTCCCGGTGGGGCCCCA--GGG 1484
                                                  -----GGGTTTGGC 1412
                         1308 GCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human T139 protein coding sequence.
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This represents the coding sequence of the numen 1129 polypeptide can be expressed by standard recombinant methodology.

The T139 polypeptide can be expressed by standard recombinant methodology.

The T139 colNA insert is deposited with ATCC under accession number

therefore the permitted of the sequence of the information of differentiative disorders, e.g. of the immune system. They can be used to differentiative disorders, e.g. of the immune system. They can be used to differentiative disorders, e.g. of the immune system. They can be used to decrease spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat disorders related to defects in sperm-egg spermatogenesis or to treat disorders related to defects in sperm-egg tusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating polypeptide activity. The polypericular processing the polymucleotides which may be useful for electing the polymucleotides in a sample, gene mapping; identifying cetting the polymucleotides in a sample, gene mapping; identifying cetting the polymucleotides in a sample, gene mutated or deleted to identify subjects at risk for or having a disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate/prevent T139 expression.
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                                                                                                                             This represents the coding sequence of the human 1139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 ATGCIGCATCCAGAGACCICCCCTGGCCGGGGGAICTCCTGGCTGTGCTCCTGGCCCTC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Gaps
Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                            Claim 2; Page 114; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                            AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 1202
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             1201 GACAACCAC-------GGGTTTGGCAACTGCGTGG 1233
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GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT 782
                                                    GCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA 842
                                                                  843 CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCTGGCTACACGGGCAGATACTGC 902
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                       CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1443 TGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCCAGGGTCC 1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #12148.
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The invention relates to isolated polynucleotide (I) and proposed (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, comparese chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags (I) if identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical color states expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capporation, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cold sequences. AsSet197-AsSet564 represent novel human DNA and sequences as based or this patent did not appear in the printed security in expension or intentity from MIPO at the expense or the invention of colding sequences or the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 IGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGGGGGCTTGGCGTCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.4%; Score 889.4; DB 23.93.4%; Pred. No. 5.9e-204;
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                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 12148; 103pp; English.
                                                                                                                                                    Tang YT;
30-MAR-2001; 2001WO-US08631.
                                      31-MAR-2000; 2000US-0540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 929; Conservative
                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                      WPI: 2001-639362/73.
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                                                                                                       (HYSE-) HYSEQ INC.
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1143 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 1202
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                                                                                                                                                                                                                                                                           GICIGIGACAICGGCIACGGGGAGCCCAGIGIGCCACCAAGGIGCAIITIICCCIICCAC 1022
                                                                                                                                                                                                                                                                                                                            ACCIGIGACCIGAGGAICGACGGAGACIGCIICAIGGIGICIICAGAGGCAGACACCIAI 1082
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547 CIGGGCIGIGGGCGCCCCIGIGCICICGCAGGCCAGGCAGCGAIAGAAGCCITIGICIGI 606
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                                      723 GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT
                                                                                     783 GCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA
                                                                                                                                                                           CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC
                                                                                                                                                                                         CAAGTGAGGTGCAGCTGCAGTGTGCACGCCGGTTCCGGGAGGAGGAGGAGCTCGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #12147.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and its binding partners are useful in medical inaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in casponal partners are useful for treating disorders involving aberrant formapping, identification of mutations capanish for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. Score 766.6; DB 23; Length 906; Similarity 95.2%; Pred. No. 1.7e-174; D1; Conservative 0; Mismatches 39; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 906 BP; 175 A; 294 C; 286 G; 151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                       Claim 1; SEQ ID No 12147; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 801; Conservative
                                                                                 biodiversity
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544 GTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGTGGGGCCACCTCAAGCCAGC 603

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The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA66691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein and the nucleic prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis; tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
               607
                                                    CCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGG 723
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GTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATG
                                                                                                                                                                                                 CAGGGGGGT-CTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA
                                      TGGGCTGTGGGCGCCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian carcinoma antigen polynucleotide SEQ ID NO:321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frudakis TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid encoding it, useful for the diagnosis, cancer, preferably ovarian cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic portion of an ovarian carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 177; 299pp; English.
                                                                                                                                                                                                                                                                                                                                             AAA70010 standard; cDNA; 690 BP.
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98US-0216003.
99US-0338933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US30270
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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23-JUN-1999;
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TCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1143 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1203 GACAGTGACTTCGAGAACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTTTTCAGAGGCAGACACCTATT 1083
                                                                                                                                                                                                                                                                                                                                                                                                         421 CCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTATT 480
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                                                                                                                                                                                   843
                                                                                                                                                                                                                                                     181 CAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGAC 240
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                                                                       GTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATG
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                                                                                                                                                                                                                           CAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGAC
                                                                                                                                                                                                                                                                                844 GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCC
                              ij
  DB 21; Length 690;
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35.9%; Score 672.8; DB 21 99.3%; Pred. No. 5.5e-152;
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                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1263 TCCTTCCGCTGGGCCACAGGGGAGCACCAG 1292
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                             Matches 685; Conservative
                Similarity
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  Query Match
                 Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         portion of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an immune response in a patient and treating ovarian cancer. This sequence represents DNA related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAG-AGCCAGGATGAAATGTCAGAGGAAGGCGGGGTGCTGGCCCCAGATCAAGAGCCAG 1142
                                                                                                                                                                                                                                                                           Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604 TGGGCTGTGGGCGCCCCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTG 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                        Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCTCAACATCAGCACCTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          664 CCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCATCATAAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to polypeptides comprising an immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.9%; Score 672.8; DB 24; Length 690; 99.3%; Pred. No. 5.5e-152; Live 0; Mismatches 4; Indels 1;
                                                                                                                                                                        Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
                                                                                                                                                                     Fling SP, Retter Hill P, Albone E;
                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 296; 408pp; English.
                                                                                                                                                                     Algate PA,
Carter D,
2000US-0617747.
2000US-0636801.
2000US-0667857.
2001US-0827271.
2001US-0884441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.3
Matches 685; Conservative
                                                                                                                                                                     Mitcham JL, King GE,
Reed SG, Vedvick TS,
                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                 WPI; 2002-164781/21
17-JUL-2000; 10-AUG-2000; 20-SEP-2000;
                                                             04-APR-2001;
18-JUN-2001;
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ACAGAAGCCAGGATGAAATGTCAGAGGAATGGCGGGGTGCTGGCCCAGATCAAGAGCCAG

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GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC 1262
                 TCCTTCCGCTGGGCCACAGGGGAGCACCAG 1292
                                                                                                                                             December 28, 2002, 17:01:35
                                                                                 TCCTTNCGCTGGGCCACAGGGGAGCACCAG
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                         2054640 seqs, 14551402878 residues
                                                                                                          US-09-944-896-49_COPY_201_447
247
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Maximum Match 100%
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                        IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ion	AX191493 Sequence AX191503 Sequence AX1933339 Homo sapi	Macaca Homo s	TOWN C	Ĕ O	Pan	HOM	HOH C	Pan	Hom	Mus	AC098076 Rattus no	Homo s Sequen	AX235371 Sequence	AX358802 Sequence	AX362295 Sequence	AX235369 Sequence	AX235373 Sequence AX235375 Sequence	Sequenc	AL136861 Homo sapı AX285067 Sequence	Sequenc	sequenc Homo sá	Sequence	Sit	٠	Homo Pseud	is:	Human		: :	linear PAT 15-AUG-2001			Vertebiata; Eutereostomit; ; Hominidae; Homo.	s and dnas encoding these
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lt o. Se	1 0 0 0	, -	•			11	13.	 	16		7 •	_ ~		- 10	٠٠ ٠	- m	m C) -	32) e # 1	3.5 3.5	. ~ .	ກດ	. 0	41	43	4. r.		RESULT 1 AX191493	LOCUS DEFINITION ACCESSION	VERSION	SOURCE	REFERENCE	TITLE

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polyA_signal
polyA_site
BASE COUNT 78
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1775)
Kato,S. and Kimura,T.
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Patent: WO 0149728-A 15 12-JUL-2001;
Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
Location/Qualifiers
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Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
Location/Qualifiers
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Pred, No. 1.8e-46;
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Sequence 25 from Patent WO0149728.
                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
a 420 c 414 g 247
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/db_xref="GI:15209690"
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Submitted (09-JUL 2002) 1, D-85764 Newherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz=heidelberg.de;
Sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZD686E1934) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sfi; host
DH10B; sites SfilA + SfilB"
/dev_stage="adult"
3171. 3176
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HOMO Sapiens mRNA; CDNA DKF2p686E1934 (from clone DKF2p686E1934).
AL833339
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ottenwaelder, B., Obermaler, B., Mewes, H.W., Weil, B., Amid, C. and
                                                                             61 GAGAGITICITGCICCICICCTGCACAACCGCCIGCGAGCIGGGICCAGCCCCCTGCG 120
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       Indels
  0; Mismatches
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/clone="DKFZp686E1934"
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246; Conservative
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LUBLISTED TOTATO PMEDISS-FL3 (Acc.No. AB009864)

R. Sitel: Draill (CACTGTGT)

R. Sitel: Draill (CACTGTGT)

R. Sitel: Draill (CACTGTGT)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 13-JUN-2001
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2 (bases 1 to 2900)

2 (bases 1 to 2900)

Direct Submission

Submitted (17-APR-2001) Katsuyuki Hashimoto, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                 181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG 240
                                                                                                                                                                                                         452 GCCCTCTGTGGAACCCCGAACCCGGGCTGGCGCCCGTGGCGCACCTGCAAGTG 511
121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
                                        oligo capping; fis (full insert sequence).
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA, clone_lib:macaque brain cDNA library QccE clone:QccE-21387.
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis brain cDNA clone: OccE-21387, full insert
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/clone_lib="macaque brain cDNA library QccE"
/dev_stage="adult"
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/protein_id="BAB41141.1"
/db_xref="GI:13676427"
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Location/Qualifiers
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/clone="QccE-21387"
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AB060195.1 GI:13676426
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PRI 27-JUL-2001
/translation="MLHSETSPGRGHLLAVLLAFLGTTWAEVWPPQLQBQAPMARALT
RKESFLLLSHNRLRSWYQPPAADMRRLDWSDSLAQLAQARALCGPPPSLASAPWH
TLQVGWWYQLLDAGSASFVEVVSLMRABGQRYSHAAGECARNATCTHYTQLWAATSSQ
LGCGRHLCSADQAATEAFVCAYSPGGNWEVNGKTIVPYKKGAMCSLCTASVSGCFKAM
DHAGGLCGECWRAQSGDPGVGVAASYWAVPEAPTLSTQGGSCPACWEETLFSESPPPL
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                                                                                                            TRGPQEPLSHELPEPRTSQHQHLPLPLSTWLHWQVLPSAVQPAVCARPVSGGGVLVRL
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Submitted (27-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                  61 GAGAGTTTCTTGCTCCTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                           121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
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On Jul 27, 2001 this sequence version replaced g1:9256116.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                    Length 2900;
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                                                                                                                                                                                                                                                                   10; Indels
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Quality: Phrap Quality >=40 99.8% of Sequence;
                                                                                                                                                                                                                       Score 231; DB 9;
Pred. No. 3.3e-43;
0; Mismatches 10;
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                       Query Match 93.5%;
Best Local Similarity 96.0%;
Matches 237; Conservative (
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SHGC-32146 G27136
SHGC-36058 G30050.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 177479)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (05-JaN-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 177479)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submitsion
Submitted (28-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Malnut Creek, CA 94598, USA
On Feb 28, 2002 this sequence version replaced gi:18071320.
Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177479)
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                                                                                                                                                                                                                                                   Homo sapiens chromosome 16 clone RP11-572F4, complete sequence. AC009153
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                                                                                                                                             44.0%; Score 108.8; DB 9; Length 163427; 98.2%; Pred. No. 2e-15; ative 0; Mismatches 2; Indels 0; (

        QY
        196
        CCAACCCGAACCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTGGGCTGGA
        247

        DD
        46068
        CCAACCCCGAGCCTGGCGTCCGGCCTGTGGCGCACCCTGCAAGTGGGCTGGA
        46119

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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                             38913 c 40421 g 42501 t
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39618 c 40894 g 49859 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-252A24"
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/chromosome="16"
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1. .177479
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DOE Joint Genome Institute.
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Unpublished
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Homo sapiens
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linear PRI 04-AUG-2000
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Direct Submission Institute and Stanford Human Genome Center. Burnett Submission DoE Joint Genome Institute, 2800 Mitchell Chive, Walnut Creek, CA 94598, USA On Aug 4, 2000 this sequence Version replaced gi:9256118.

Draft Sequence Produced by DOE Joint Genome Institute
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1 (bases 1 to 180596)

DOE Joint Genome Institute and Stanford Human Genome Center.

Unpublished
                                                                                                                                                     AC009060 180596 bp DNA linear PRI 04-AUG-20
HOMO Sapiens chromosome 16 clone RP11-296110, complete sequence.
AC009060
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PROGRESS ***, 10 unordered pieces.
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        QY
        196
        CCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCCCCTGCAAGTGGGCTGGA
        247

        DD
        135047
        CCAACCCCGAGCCTGGGCTCGGCCTGTGCGCCACCTGCAAGTGGGCTGGA
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Fullity: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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48046 a 43474 c 42543 g 46533 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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AC126771.1 GI:21717140
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WI-16981 G21928
WI-9564 G06056.
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                                                                                                                                                                                                                       Direct Submission
Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                   sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 191546 bases at least Q40
Consensus quality: 193703 bases at least Q30
Consensus quality: 194840 bases at least Q20
Estimated insert size: 0; null estimation
Estimated insert size: 196560; sum-of-contigs estimation
Quality coverage: 2.1474836E7 in Q20 bases; null estimation.

* NOTE: This is a 'working draft' sequence. It currently
* Consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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50025 a 47482 c 47491 g 51562 t 900 others
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93612: contig of 23383 bp in length
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70129: contig of 23317 bp in length
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5809: gap of unknown length
7800: contig of 1991 bp in length
7900: gap of unknown length
7727: contig of 6827 bp in length
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contig of 1766 bp in length
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/db_xref="taxon:9606"
                                                                                                                                   Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: RPCI-11_396D24
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14827: gap of unk
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Center Code: JGI
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                                                                                            1 (bases 1 to 197460)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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Consensus quality: 156671 bases at least Q40
Consensus quality: 183548 bases at least Q30
Consensus quality: 188691 bases; sum-of-contigs estimation
Bstimated insert size: 199144; sum-of-contigs estimation
Quality coverage: 3.4 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 60 contigs. The true order of the places

* is not known and their order in this sequence record is

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                 HTG 21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Jun 21, 2000 this sequence version replaced gi:7689944.
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                        AC009125 205044 bp DNA linear HTG 21 HOMO Sapiens chromosome 16 clone RP11-492H8, WORKING DRAFT SEQUENCE, 60 unordered pieces.
                          Db 125694 CCAACCCCGAGCCTGGGGTCCGGCCTGTGCACCTGCAAGTGGGCTGGA 125745
196 CCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTGGGCTGGA 247
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Sequencing of Human Chromosome 16
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

1 (bases 1 to 200409)

S Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Buhay, C., Burch, P., Burkett, C., Brown, M., Bryant, N.P.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
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Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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Pan troglodytes clone RP43-53A2, WORKING DRAFT SEQUENCE, 14
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,

Gabisi, A., Gao, J., Garcia, A., Garraa, N., Gill, R.,

Gorrell, J.H., Guevara, W., Garnartne, P., Hale, S., Hamilton, K.,

Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,

Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,

Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,

Kratisson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Kratovic, J., Kureshi, A., Landry, M., Leal, B., Lewis, L.C., Lewis, L.

Lozado, R.J., Lichtarge, O., Lieu, C., Liu, W., Loulseged, H.,

Lozado, R.J., Li, R., Mapus, P., Marting, R., Martinez, E.,

Maneshwari, M., Mapus, P., Mitchell, T., Wordbat, R., Martinez, E.,

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Moser, M., Nal, D., Newtson, N., Newtson, N., Nguyen, A., Nguyen, N.,

Oragunye, N., Oviedo, R., Parine, E., Patch, C., Culles, M., Ren, Y.,

Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,

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Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Tamerisa, R., Tanney, K.,

Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wallington, S.,

Whole, W., Wuy, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,

Weller, W., Wuy, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 200409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On Jun 21, 2002 this sequence version replaced gi:21450389.
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Sequencing vector: Plasmid; M77789
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Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 177595 GGCCCCAGGACTGACAGCCTGGCCCAACTGGCTCAAGGCCAGGCACCCCTGTG 177536
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 GGAGGCTGGACTGGACTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTG 190
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-396D24
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/organism="Pan troglodytes"
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Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Peters, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stanger Thomann, N., Tirrell, A., Vassiliev, H., Yiel, R., Yoo, A., Talamas, J., Tesfaye, S., Theodore, J., Zimmer, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                               Direct Submission
Submitted (12-JAN-2000) Whitehead Institute/MIT Center for Genome Seearch, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6730807.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
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* Sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5885
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6016: gap of 100 bp 100 bp 27914: contig of 898 bp in length 7014: gap of 100 bp 27910: contig of 896 bp in length 8010: gap of 100 bp 
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92: gap of 100 bp
1883: contig of 891 bp in length
83: gap of 100 bp
20885: contig of 902 bp in length
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32866: contig of 885 bp in length
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13022 43934: contig of 913 bp in length
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21899: contig of 914 bp
99: gap of 100 bp
22919: contig of 920 bp
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. I (bases I to 204182)

Si (bases I to 204182)

Ruzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Buck, J., Burck, C., Burchl, K., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carron, T.F., Chen, S., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Cohle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, C., Edorlo, D., Davis, C., Edwards, C., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Font, J., Foster, P., Frantz, P., Gabisi, A., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
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Pan troglodytes clone RP43-35B16, WORKING DRAFT SEQUENCE, 8
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58884: contig of 882 bp in length
58884: contig of 882 bp in length
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55924: contig of 910 bp in length
                                                                                                                                                                                                                                     59895: contig of 911 bp in length
                                                                                                                                                                                                                                                                        95: gap of 100 bp 60882: contig of 887 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 107.2; DB 2;
Pred. No. 5.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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97.38;
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Best Local 5
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KEYWORDS
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Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Herlins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, E., Jacobson, B., Jah, S., King, L., Korvah, J., Jacobson, B., Jachson, B., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Karlshi, A., Landry, M., Landry, M., Lall, E., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martin, E., Martindale, A., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Marteker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N., Nidyen, N., Okwuonu, G., Oragunye, N., Orkerson, E., Nwokenkwo, S., Oragunye, N., Oradoo, R., Pace, A., Payton, B., Sepery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu'L. L., Gisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Sutchon, A., Tamerisa, R., Tangy, H., Tansey, J., Taylor, C., Tanger, P., Tanger, R., Tanger, R., Tanger, R., Washington, S., Wall, R., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weirston, R., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). ONDE: This is a "working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990129
Consensus quality: 202604 bases at least Q40
Consensus quality: 204032 bases at least Q40
Consensus quality: 205104 bases at least Q30
Estimated insert size: 200244; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 9.4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of unknown length
contig of 41350 bp in length
gap of unknown length
contig of 34346 bp in length
gap of unknown length
contig of 20281 bp in length
gap of unknown length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length contig of 27892 bp in length
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contig of 13171 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: ZUAY
Center clone name: RP43-35B16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
2 (bases 1 to 204182)
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124988:
145269:
145369:
173261:
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186532:
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124989
145270
145370
173262
173362
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Query Match

AC026468/c DEFINITION

ACCESSION

KEYWORDS VERSION

SOURCE

RESULT 13

δλ g ORGANISM

REFERENCE AUTHORS JOURNAL REFERENCE

TITLE

TITLE JOURNAL

REFERENCE AUTHORS JOURNAL

COMMENT

AUTHORS

source

FEATURES

BASE COUNT

ORIGIN

FEATURES

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49567 a 43464 c 41958 g 44686 t
                        /organism="Homo sapiens"
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DOB Joint Genome Institute.
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                                            /db_xref="taxon:9606"
/chromosome="16"
                                                                                          /clone="RP11-419C5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="16"
/clone="RP11-106J23"
91050. ,91410
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DOE Joint Genome Institute.
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                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                            Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                  Query Match
                                                                                                         BASE COUNT
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VERSION
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DDE Joint Genome Institute.

Direct Submission

Submitted (02-Nov-2001) Production Sequencing Facility, DDE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA Sequence Quality Assessment:

This entry has been annotated with Sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality estimates above 40 are expected to have less than Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU26468 179675 bp DNA linear PRI 02-NOV-2001
Homo sapiens chromosome 16 clone RPI1-419C5, complete sequence.
ACU26468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179675)
DOB Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                           This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                     136 CTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATC 195
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                               Query Match
43.4%; Score 107.2; DB 2; Length 204182;
Best Local Similarity 97.3%; Pred. No. 4.4e-15;
Matches 109; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
186632: gap of unknown length
201672: contig of 15040 bp in length
201772: gap of unknown length
204182: contig of 2410 bp in length.
                                                                                                                                                                                                                    726 others
                                                                                                                                                                                                        52711 a 50970 c 50521 g 49254 t
                                                                                                                                         /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                          Location/Qualifiers
                                                                                                                                                                                  /clone="RP43-35B16"
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DOE Joint Genome Institute.
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201773
                        186633
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Direct Submission

Submitted (07-FEB-2002) Production Sequencing Facility, DOE Joint
Submitted (07-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 7, 2002 this sequence version replaced gi:16924076.

This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASSUI file.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 190595)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                  46561 CAGGACTGGAGTGACAGCCTGGCCCAGCTCAAGCCAGGCAGCCCTCTGTGGAACC 46502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACUUSUZZ 190595 bp DNA linear PRI 07-FEB-2
Homo sapiens chromosome 16 clone RP11-106323, complete sequence.
AC009922
                                                                                                                                        136 CTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATC 195
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42.8%; Score 105.6; DB 9; Length 179675; llarity 96.4%; Pred. No. 1.1e-14; Conservative 0; Mismatches 4; Indels 0; 6
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mammatia; wttnerla; rrimates; Catarrini; Homilidae; Fah.

I (bases 1 to 191108)

Muzny, D.M., Adams, C., Ado-Oduola, B., Ali-Osman, F.R., Allen, C., Ashabord, S.L., Amaratunge, H.C., Arel, Banks, T., Barbaria, J., Babroto, J., Bingae, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Benton, J., Briega, M., Brown, E., Brown, M., Brytant, N.P., Buhay, C.,

Burch, P., Briega, M., Brown, E., Brown, M., C., Chen, G., Chen, R., Charch, T., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,

Day, Carroll, L., Daderich, D.A., Delaney, K.R., Delgado, O.,

Denn, A.L., Ding, Y., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elbajc, P., Frantz, P., Gabisi, A., Garcia, A., Garner, T., Forster, P., Rantz, P., Gabisi, A., Gaveria, W., Havlak, P., Hake, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hake, S., Hamilton, K., Marris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, L.E., Jackson, E., Lui, J., Li, Z., Lichtarge, O., Lieu, C., Liu, Y., Liu, W., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, Y., Liu, M., Martinez, E., Mashiney, B., Martin, R., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG 25-0CT-2001
                                                                                                                                                                                                                                                                                                           Db 188925 CAGGACTGGAGTGACAGCCTGGCCCAGCTGGCTCAAGCCAGGCACCCTCTGTGGAACC 188866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                    136 CTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCCAGCCCTCTGTGGAATC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC097265
Pan troglodytes clone RP43-119N13, WORKING DRAFT SEQUENCE, 4
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HTG; HTGS_PHASEI; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      DD 188865 CCAACCCCGAGCCTGGCGTCCGGCCTGCGCCCTCCCAAGTGGGCTGGA 188814
                                                                                                                           Score 105.6; DB 9; Length 190595; Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                          196 CCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTGCAAGTGGGCTGGA 247
                                                                                                                                                                                                        4; Indels
       /note="unresolved tandem repeat"
51435 a 43243 c 43697 g 52220 t
                                                                                                                                                                                                        0; Mismatches
                                                                                                                                            42.8%;
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Unpublished
                                                                                                                                                                                                            Matches 108; Conservative
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                                                                                                                                                                            Local Similarity
                                                                                                                                                Query Match
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AC097265/c
                                             BASE COUNT
ORIGIN
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(bases 1 to 191108)

2 (bases 1
Worley, K.C.

AUTHORS

REFERENCE

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NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990129
Consensus quality: 191814 bases at least Q40
Consensus quality: 194113 bases at least Q20
Consensus quality: 194113 bases at least Q20
Estimated insert size: 193275; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
Direct Submission
Submitted (13-0CT-2001) Human Genome Sequencing Center, Department
Submitted (13-0CT-2001) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 23, 2001 this sequence version replaced gi:16258969.

Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
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                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uuery Match 42.1%; Score 104; DB 2;
Best Local Similarity 95.5%; Pred. No. 2.4e-14;
Matches 107; Conservative 0; Mismatches
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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                     Center clone name: RP43-119N13
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                                                                                                                                                                                                                                                                                                                            Center project name: ZUAR
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W79362 BI759353 BI759735 AI522123

AA527105 AL040183 AI245843

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     GenCore version 5.1.3
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                                                             16154066 seqs, 8097743376 residues
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                   - nucleic search, using sw model
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468 9 AA734254 470 9 AI771208 481 10 AR061065 491 9 AI32426 505 9 AA017773 505 9 AA017773 507 10 AW051065 508 11 AW251268 507 10 AW251268 507 11 BP7747414 514 12 BP7747414 514 12 BP7747414 524 1 AB773653 525 9 AI777458 526 17 AZ73529 527 19 AZ73639 643 13 BP7767610 528 17 AZ75788 640 12 BE673052 641 10 AR081382 642 14 BQ165289 643 12 BE6770943 643 12 BE6770943 644 14 BQ1652363 645 12 BG770943 647 12 BG770943 648 11 BC077020 649 12 BE686972 640 13 BF7155363 641 10 AV0813562 641 10 AV0813562 641 10 AV081364 642 14 BQ122418 72 14 BQ1224468 884 14 BQ722311 72 14 BQ1221455 910 13 BI771269 911 13 BI77104 81 13 BI77107 81 13 BY77507 110 10 AW081341 110 10 AW081341 110 110 AW08134 111 BR775507 113 BG75891 113 BG75801 113 BG75801 114 BY77507 115 BF442688 113 BR775507 113 BR77507 113 BR77507 113 BR77507 113 BR77507 113 BR77507 113 BR77507 113 BR77507 113 BR77507 113 BR77507 114 BY77507 115 BR776391 117 BR776391 118 BR776391 119 BR776391 119 BR776391 110 AW0817462 111 BR776391 111 BR776391 111 BR776391 112 BR776391 113 BR776391 113 BR776391 114 BR776391 115 BR776391 117 BR776391 118 BR776391 119 BR776391 110 AW081782 111 BR776301 111 BR776301 112 BR776301 113 BR776301 113 BR776301 114 BR776301 115 BR776301 117 BR776301 118 BR776301 119 BR776301 111 BR776301 111 BR776301 111 BR776301 112 BR776301 113 BR776301 113 BR776301 114 BR776301 115 BR776301 117 BR776301 118 BR776301 119 BR776301 111 BR776301 111 BR776301 111 BR776301 112 BR776301 113 BR776301 114 BR776301 115 BR776301 117 BR776301 118 BR776301 119 BR776301 111 BR776301 111 BR776301 111 BR776301 112 BR776301 113 BR776301 114 BR776301 115 BR776301 117 BR776301 118 BR776301 118 BR776801 119 BR776801 111 BR776801 111 BR776801 111 BR776801 111 BR776801 112 BR776801 113 BR776801 114 BR776801 115 BR776801 117 BR776801 118 BR776801 118 BR776801 119 BR776801	
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BG321803 A1013913 BQ180952 BQ180952 BQ773110 B1197752 BM541116 BB552596 BB552596 BG7141674	D0141024 AQ341023 BM677386 AQ325182 AV918387 BF723810 BF723810 BF723840 AV300908 BM682559 AL036834 BQ767081	BQ181354 BQ183750 BQ183750 BQ183750 BQ18129 BQ18129 BM975548 BM990368 BM990342 BC5737842 BQ5737842 BQ5737842 BQ5737842 BQ5737842 BQ5737842 BQ5737842 BQ5737842 BQ176255 BQ176255 BQ183051 BQ183051 BQ183051 BQ183051 BQ183051 BQ183051 BQ183051 BQ183051 BQ183051 BQ183051	ALIGNMENTS 645 bp 5', mRNA seg
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0	9967 9968 9970 972 974 976 976	00000000000000000000000000000000000000	RESULT 1 BM695392 LOCUS DEFINITION UI-E- ACCESSION BM699 VERSION BM699

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BM695392

OI.E-CQ1-aev-n-19-0-UI.I UI-E-CQ1 Homo sapiens cDNA clone
UI-E-CQ1-aev-n-19-0-UI 5', mRNA sequence.

BM695392

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GI:19008650

EST.

BM695392.

GI:19008650

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BMMmmalia; Eutheria Primates; Catarrhini; Hominidae; Homo.

I (bases I to 645)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Mormalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medwa

451 Eckstein Medwa

Tel: 319 335 8250
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REFERENCE AUTHORS

TITLE JOURNAL MEDLINE

COMMENT

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/(tissue_type="Optic nerve"
//dev_stage="adult"
//dev_stage="adult
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencidy by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 Reverse.
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/clone="UI-E-CQ1-aev-n-19-0-UI"
/clone_lib="UI-E-CQ1"
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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BM547887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 725 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
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                                                                                                                                                                                                                                                                                                        AI307814 617 bp mRNA linear EST 08-APR-1999 tb28d11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055669 3' similar to TR:Q61830 Q61830 MANNOSE RECEPTOR, C TYPE 1 PRECURSOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
                                                                               1252 CCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCT 1311
1192 ACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGA 1251
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                                                                                                  /clone="IMAGE:2055669"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
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Pred. No. 1.8e-161;
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100.0%; Pred. No. 1...
0; Mismatches
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/lab_host="DH10B"
                                                                                                                                                                1312 TTGGGCAGCCTGACAACCACGGG 1334
                                                                                                                                                                                        601 TTGGGCAGCCTGACAACCACGG 623
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .617
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AGENCOURT_6531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633 BM547887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nobert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                        1719 AGATGGGCTTCAATTAGATGGCGAAGGAGGACACCGCCAGTGGTCCAAAAAAGGCTGCT 1778
                                                                                                                                                                                                1539 TTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCC 1598
                                                                                                                                                                                                                                                                                            1599 AAAGAGGTCTCAGACCTTGCACAATGCCAGAAGTTGGGCAGAAGAGGCAGGGAGGCCAG 1658
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                                                                                                 NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                       133 TTACCTGTCTGCCCACCTGTCTGGAACAAGGCCAGGTTAAGACCACGTGTGCCTCATGTCC 273
                                                                                                                                                                                                                                                                                                                             152 AGATGGGCTTCAATTAGATGGCGAAGGAGGAGGACCCCCCCGGTGGTCCAAAAAGGCTGCT
                                                                                                                          1912 CCAGGGTCCTGAGGCCTGACCATGGCTCCCTCGCCTGGCCTGGGAGCACGGCTCTGC
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/lab_host="DH10B"
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/organism="Homo sapiens"
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/clone_lib="NIH_MGC_124"
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Query Match
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                 TITLE
JOURNAL
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                                        COMMENT
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insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 578)
                                                                                                                                76 GGCIGAGCCAGGCIGIGCACGGAGCACCIGACGGGCCCAACAGACCCAIGCTGCTACAG 135
                                                                                                                                                                                                           136 AGACCICCCTGGCCGGGGGATCTCCTGGCTGTGCTCCTGGCCCTTGGCACCACCT 195
                                                                                                                                                                                                                       GGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACA 255
                                                                                                                                                                                                                                                                  GGAAGGAGAGTITCITGCICCTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCC 315
                                                                                                                                                                                                                                                                                                           CTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCA 375
                                                                                                                                                                                                                                                                                                                                                         GGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGC 435
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                                                                            27.3%; Score 512; DB 13; Length 1076; 99.5%; Pred. No. 1.3e-161; tive 0; Mismatches 3; Indels 0
                                               6 others
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                                            338 g
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                                                                                      Similarity
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                                          BASE COUNT
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Note="Weetcr: pCMV-SPORT6 (Life Technologies); Site_1:
NotI: Site_2: Sall; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TGGACCAGGCGTGG-3 and
5'-TGACTAGTTGTAGATGGGAGGGGCGCCCT(15)-3'. Size selected >
1'Nb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and doneted by J. Lupski, M.D.Ph.D. (Baylor College of Medicine); available through Life
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                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
   Tissue Procurement: Dr. James R. Lupski
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Agencourt Bioscience Corporation
   Clone distribution: MGC clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
   Plate: LLAM13592 row: d column: 08
   High quality sequence stop: 542.
   Location/Qualifiers
   I. 578
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 CCAGGGTCCTGAGGCCTGACCACATGCTCCCTCGCCTTGGGAGCACCGGCTCTGC 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:6191575"
/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/tissue_type="Osteoarthitic Cartilage"
/tissue_type="Osteoarthitic Cartilage"
/dev_stage="Addlut"
/lab.host="DHIOB (Life Technologies)"
/lab.host="DHIOB (Life Technologies)"
/note="Organ: Rnee; Vector: pT773-pac (Pharmacia) with a Modified polylinker; Site_1: ECOR I; Site_2: Not I; modified polylinker; Site_1: ECOR I; Site_2: Not I; modified polylinker; Site_1: BCOR I; Site_2: Not I; modified polylinker; Site_1: Bcortaing the Not I cartilage The library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEBAIL: CGAPDS-redmail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
firom Dr. M. Bento Soares, bento-soares@ulowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 29-MAY-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 612)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      612 bp mRNA linear EST 29-MAY.
UI-H-EUI-bac-n-13-0-UI.s1 NCI_CGAP_Ct1 Homo sapiens cDNA clone
UI-H-EUI-bac-n-13-0-UI.3', mRNA sequence.
                                                             (df)18 tail. The sequence tag for this library is
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/clone_lib="NCI_CGAP_Ct1"
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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Seq primer: -40UP from Gibco
Bigh quality sequence stop: 446.
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                                                                                                                                                          7k17b07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3444444 3' similar to SW:MANR_HUMAN P22897 MACROFHAGE MANNOSE RECEPTOR PRECURSOR. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1539 TTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCC 1598
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCL_CGAP_GC6"
/tissuc_type="pooled germ cell tumors"
/lab_host="DH10B"
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                      /organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Emmert-Buck, M.D., Ph.D.
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BF057185.1 GI:10811081
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Contact: Robert Strausberg, Ph.D.
Email: gapbs.r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                   1359 GGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGC 1418
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UI.H-EII.aza-p-20-0-UI.sl NCI_CGAP_EII Homo sapiens CDNA clone
NUMBE:5846275 3', mRNA sequence.
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                                                      Length 612;
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                                              Score 427; DB 14;
Pred. No. 4.8e-133;
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/db_xref="taxon:9606"
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                                              22.8%;
99.8%;
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                                                                    Matches 477; Conservative
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/clone="IMAGE:5846275" /clone_lib="NCI_CGAP_EI1"

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xs48f01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2772889 3' SIMILAT to SW:MANR_HUMAN P22897 MACROPHAGE MANNOSE RECEPTOR AND A Sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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99.8%; Pred. No. 4.2e-133;
live 0; Mismatches 1;
/tissue_type="Chondrosarcoma"
                                                                                                                                                                                                                           TAG_LIB=UI-H-EI1
TAG_TISSUE=chondrosarcoma
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                                                                                                                                                                                                                                                      TAG_SEQ=ACACTTGCAC"
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                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-blo.llnl.gov/bbrp/lmage/image.html
Seq primer: -400P from Gibco.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                  Tumor Gene Index
Unpublished (1997)
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/tissue_type="pooled germ cell tumors"
/tissue_type="pooled germ cell tumors"
/lab_host="bolloB"
/lab_host="bolloB"
/lab_host="bolloB"
/note="wector: pT713D-pcc (pharmacia) with a modified
/note="wector: pT713D-pcc (pharmacia) with a modified
polylinker; Site_1: Not I: Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
from the normalized library NCI_CGAP_GC4 was prepared
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs)
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
  EST 05-FEB-2001
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG150347
7j99a09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442841 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1666 CAGGGAGTGAGTGTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTGATTGGGAAGATGGG 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1426 CCCGAAACCGTTACATCTGCCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCCAGGGT 1485
                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.0%; Score 413; DB 12; Length 44
100.0%; Pred. No. 2.8e-128; Lindels
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_GC6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -400P from Gibco
High quality sequence stop: 446.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R. Emmert-Buck, M.D., Ph.D.
                                                                                                               BG150347.1 GI:12662377
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                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                   mRNA sequence.
BG150347
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                                                                                                                                                                                                                               AW001740 490 bp mRNA linear EST 08-MAR-2000 ws04c06.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496202 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: M.T.-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
Insert Length: 846 Std Error: 0.00
Seq Primer: 400P from Giber: 0.00
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
                                   1726 CTTCAATTAGATGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCC 1785
                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
200 CAGGGAGTGAGTGTTAGAAGAAGCTGGGGCCCTTCGCCTTTTGATTGGAAGATGGG 141
                                                    1376 GGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACG 1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                     DB 10; Length 490; 6.1e-120;
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/clone="IMAGE:2496202"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                 mRNA sequence.
AW001740
AW001740.1 GI:5848656
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Unpublished (1997)
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/db_xref="taxon:9606"
/clone="IMAGE:306081"
/clone="IMAGE:306081"
/clone="IMAGE:3060881"
/clone="IMAGE:3060881"
/clone="taxon:9606"
/clone="taxon:9606"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT773D-pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; NoI_CGAP_Sub5
is a subtracted library derived from NOI_CGAP_Sub4. The
NCI_CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NOI_CGAP_sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NOI_CGAP_Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs
1322376-1323911, 1456008-1456775,1500552-1502855);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 460)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UI-H-BI3-alt-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone AM451907.1 GI:6992683
1496 GACCACATGGCTCCCTCGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACC 1555
                                                                                            1556 TGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCT 1615
                                                                                                                                                                                            1616 TGCACAATGCCAGAAGTTGGGCAGAAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGA 1675
                                                                                                                                                                                                                                                                                      1676 GTGTTAGAAGAAGCTGGGGCCCTTCGCCTTTTGATTGGGAAGATGGCCTTCAATTAG 1735
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                                                                                                                                                                                                                                                                                                                                                                                                                  I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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AW451907/c
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NCI_CGAP_Kid5 pool 1 LLAM 3338-3342,3722-3725, 3776-3778 (IMAGE CloneIDS 1323912-1325831, 1471368-1472903, 1492104-1492355); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDS 1414920-1417991,1520904-152439); NCI_CGAP_EG4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CLONEIDS 1257096-1258631,1469064-1470983, 1475592-1476743); NCI_CGAP_PE22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CLONEIDS 985608-986759, 2758-2759, 3062-3068 (IMAGE CLONEIDS 985608-986759, 1101192-11011955), 1217928-1220615); NCI_CGAP_COLO pool 1 LLAM 2644-2653, 281-2872 (IMAGE CLONEIDS 1057416-106525), 1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE CLONEIDS 2710616-2710535) and NCI_CGAP_Sub2 (IMAGE CLONEIDS 2710516-2710535) and NCI_CGAP_Sub2 (IMAGE CLONEIDS 2710516-2712455) (10% of the driver population), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CLONEIDS 2712456-2725991) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub3 (IMAGE CLONEIDS 2712456-272599) (70% of the driver population), subtraction was performed as previously described [Bonaldo and Subtraction and Subtra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 08-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1455 CAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCTCGC 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1575 GTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAGTTG 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1695 CCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGAGGACAC 1754
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TAG_LIB=NCI_CGAP_Kid3
TAG_TISSUE=kidney
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99.8%;
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// note="Vector: pT713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA iron the normalized library NCI_GCAP_GC4 was prepared, and from the normalized library NCI_GCAP_GC4 was prepared, and this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCY-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 495)
NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL TINSTITUTE, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Uppublished (1997)
                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1429 GAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT 1488
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                                                                                                                                                                                                                                                                                                                        Bonaldo, Ph.D. cDN Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
Location/Qualifiers
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/clone_lib="NCI_CGAP_GC6"
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AI792411
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
www-bio.lin.gov/bbrp/image/image.html
Insert.Length: 55 Std Error: 0.00
                                                                                                                           AI627475 509 bp mRNA linear EST 07-MAR-2000
ty80a06.x1 NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2285362 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP hybridization, this DNA was used as tracer in a subtractive from a pool of 5,000 clones made from the same library (CloneIDS 1322376-1323911, 1456007-1456775, and Fatima Bonaldo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2285362"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Unpublished (1997)
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AI627475
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/sex="pooled (6)"
/lab_host="Pooled (6)"
/lab_host="Delion"
/note="Vector: pSPORTI; Site_1: SalI; Site_2: NotI; RNA
was prepared from a pool of 6 anonymous Wilms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
light of relection. Dela Library preparation was with
the BRL/Life Tech. Superscript Plasmid system. An
oligo-dT NotI primer for first strand synthesis generated
gaggccgccc(1) at the 3' end of the clones. A 5' SalI
adaptor was used with sequence 5'-gtcgacccacgcgtccg-3'
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pSPORTI.
Library was constructed by Dr. Manfred Gessler."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 02-JUL-1999
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1 (bases 1 to 463)

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
1554 CCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGAC 1613
                                                                                                        1614 CTTGCACAATGCCAGAAGTTGGGCAGAGAGGCAGGGAGGCCAGTGAGGGCCAAGGGAGT 1673
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                                                                                                                                                                                                                                                                                                                                AGAIGGCGAAGGAGGACACCGCCAGIGGICCAAAAAGGCIGCICICITCCACCIGGCC 1793
                          an34b09.y5 Gessler Wilms tumor Homo sapiens cDNA clone
IMAGE:1700537 5' similar to TR:043692 043692 25 KDA TRYPSIN
INHEBITOR: ; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1794 CAGACCCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCAC 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:1700537"
/clone_lib="Gessler Wilms tumor"
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Seq primer: -40RP from Gibco
High quality sequence stop: 429
Location/Qualifiers
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EST 28-FEB-2002
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purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneibs 13223/6-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Ronaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 405)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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UT-E-CII-aft-b-08-0-UI.rl UI-E-CII Homo sapiens cDNA clone
UI-E-CII-aft-b-08-0-UI 5', mRNA sequence.
BM708158
BM708158.1 GI:19021416
                                                                                                                                                                            Length 494;
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                                                                                                                                                                            Query Match 17.4%; Score 326; DB 9; L4 Best Local Similarity 99.5%; Pred. No. 3.3e-99; Matches 426; Conservative 0; Mismatches 2;
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lange/image.html
Insert Length: 891 Std Error: 0.00
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NCI-GARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                     254 CAGGAAGGAGAGITICITGCICCICCTGCACAACCGCCTGCGCAGCIGGGICCAGCC 313
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                              99.7%; Pred. No. 1.5e-106; vative 0; Mismatches 1;
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/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/note="lorgan: eye; Vector: pr773-Pac (Pharmacia) with a modified polylinker: site_l: EcoR I; Site_l: Not I;
IU-E-CII is a normalized oDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, synthesis was primed with an oligo-dT primer containing a synthesis was primed with no ligo-dT primer containing a daptor, digested with Not I, and cloned directionally the synthesis of first-strand cDNA was ligated to an EcoR I alto primes for the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Wisual System, supported by National Eye Institute
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cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Seq primer: M13 Reverse.
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Similarity 99.7%; Pred. No. 3.8e-97; Length 405;
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/clone_lib="UI-E-CII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                /organism="Homo sapiens"
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pCMV-SPORT6; Site_1: Not1: Site_2: ECGKV (destroyed): Source anonymous pool of 3 colons, age 26 yo male, 49 yo stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and 70 yo female. Library is oligo-dT primed and directionally cloned (ECGKV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by Clouds. (Note: this is a NIH_MGC Library."
ENKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 836)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, ph.D.
                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 GAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCC 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 CAGCCACGCGGCAGGAGAGGTGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGT 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           584 GIGGGCCACCICAAGCCAGCIGGGCIGIGGGCGGCACCIGIGCICIGCAGGCCAGACAGC 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bmail: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 CGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.4%; Score 308; DB 13; Length 836; 99.2%; Pred. No. 2.5e-93; .ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11465 row: b column: 12
High quality sequence stop: 761.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:5186219"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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1452 GCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCT 1511
 1546 TCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGG:1605
                  123 TCTGCCCACCTGTCTGGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B
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AI827695.1 GI:5448366
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                    EST 09-JUN-1998
                                                                                                                                                                                                                                                                                                     AA903561 383 bp mRNA linear EST 09-JUN-199
ok63a05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518608 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 383)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                             824 GAGCIGCCAGAACCAIGGACGICICAACAICAGCACCIGCCACIGCCACIGICCCCCIGG 883
                                                                                                                                          764 CITCAAAGCCIGGGACCAIGCAGGGGGGCTCIGIGAGGICCCCAGGAAICCIIGICGCAI 823
704 AATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTG 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%; Score 285; DB 9; Length 383; 99.7%; Pred. No. 2e-85; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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/clone="IMAGE:1518608"
/clone_lib="NCI_CGAP_GC4"
                                                                                                                                                                                           884 CTACACGGGCAGATACTGCCAAGTGAGGTGCAG 916
                                                                                                                                                                                                            660 CTACACGGGCAGATACTGCCAAGTGAGGTGCAG 692
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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AA903561/c
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/lab.mosus - univo
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHLJ9W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
vitroer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Scares and M. Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSER Length: 759 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
High quality sequence stop: 455.
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1666 CAGGGAGTGAGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGG 1725
                                                                                                                                                                                                                             1726 CITCAAITAGAIGGCGAAGGAGAGACACCGCCAGIGGICCAAAAAGGCIGCICTITCC 1785
                                                                                                                                                wfllall.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350268 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_NFL_T_GBC_S1"
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149 c 142 g 103 t
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                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 bp
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TAG_LIB=NCI_CGAP_GC4
TAG_TISSUE=germ cell
TAG_SEQ=AAATC"
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AI863534/c
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/clone=lib="NCI_GGAP_gub3"
/clone=lib="NCI_GGAP_gub3"
/lab_host="bh108 (Life Technologies)"
/note="Vector: pT73D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_GGAP_gub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_GGAP_libraries: NCI_GGAP_col0,
NCI_GGAP_pcl0; NCI_GGAP_pris, NCI_GGAP_col0,
NCI_GGAP_Lol0; NCI_GGAP_Pris, NCI_GGAP_Lym2,
NCI_GGAP_Kid3, NCI_GGAP_Kid11, NCI_GGAP_Lym2,
NCI_GGAP_Eriz, NCI_GGAP_Kid11, NCI_GGAP_Lym2,
NCI_GGAP_Eriz, NCI_GGAP_Kid11, NCI_GGAP_Lym2,
NCI_GGAP_Eriz, NCI_GGAP_CO8, NCI_GGAP_CLII, NCI_GGAP_Leiz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 bp mRNA linear EST 29-OCT-1999 IMAGE:2716868 3', mRNA sequence.
AM137750.1 G1:6142068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Uppublished (1997)
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first tail. cDNA nibrary Preparation: M.B. Soares Lab Clone distribution information can be found through the INT-CGAP clone distribution information can be found through the INTA G.E. Consortium/Libra at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1512 CGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGC 1571
                                                                                                         1572 CAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAG 1631
                                                                                                                                                                      1692 GGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGAGA 1751
                                                                                                                                                                                                                                                                                               1752 CACCGCCAGTGGTCCAAAAAGGCTGCTCTTTCCACCTGGCCCAGACCCTGTGGGGCAGC 1811
                                                                www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                           55 GGAGCTTCCCTGTGGCATGAACCCCAC 29
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1 (bases 1 to 396)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                       1574 GGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAGTT 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1634 GGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGATGTTAGAAGAAGCTGGG 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1694 GCCCTTCGCCTGTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGAGGACA 1753
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0
                                                                                                                                                                                                                                                                                                                                14.6%; Score 274; DB 10; Length 385; 99.7%; Pred. No. 9.5e-82; 1ve 0; Mismatches 1; Indels (
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EST 25-SEP-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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603043573F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183898 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11459 row: a column: 19
                            Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray unpublished (2000)
Contact: John Quackenbush
THE Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1791 GCCCAGACCCTGTGGGGCAGCGGGGGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAAT 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 500)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1671 AGTGAGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTGATTGGGAAGATGGGCTTCA 1730
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.ini.pg
Tissue procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                         Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGL"
/ncle="Vector: pBluescriptSKm"
111 c 142 g 98 t
                                                                                                                                                                                                                                                                                                                                                                                           14.1%; Score 265; DB 10;
100.0%; Pred. No. 8.5e-79;
tive 0; Mismatches 0;
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BI761101
BI761101.1 GI:15752679
                                                                                                                                                                                     Email: johnq@tigr.org
                                                                                                                                                                                                                       Seq primer: Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 265; Conservative
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Best Local Similarity
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1 (bases 1 to 470)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. DNA Library Preparation: M.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CSAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1710 TGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGGACACCGCCAGTGGTCCAAA 1769
                                       Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1650 GGAGGCCAGTGAGGGCCAGGGAGTGATGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTT 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 GGAGGCCAGTGACGCCAGGGAGTGTTAGAAGCTGGGGCCCTTCGCCTTTT 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 14.6%; Score 274; DB 9; I al Similarity 100.0%; Pred. No. 9.3e-82; 274; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 t
                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                          High quality sequence stop: 306.
Location/Qualifiers
1..396
                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:2386307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 9
                                                                                                                                                                                                                                                       Seq primer: -40up from Gibco
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                                                                                                                    Emmert-Buck, M.D., Ph.D.
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                                     rumor Gene Index
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                                                                                                                   /note="Organ: pooled colon, kidney, stomach; Vector: pcMv-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA female, 71 yo male monymous pool of 3 colons, age 26 yo male, 49 yo source anonymous pool of 3 colons, age 26 yo male, 49 yo stomachs, 62 yo male colon; 46 yo male kidney, and pool of 2 oligo-dT primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size 1.4 kb, enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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603042530F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5182999 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AGAAACAAGCCGGGTGGGTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGATCTCCTGGCTGTGTCTCTGGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TCCTIGGCACCACCIGGGCAGAGGIGIGGCCACCCCAGCTGCAGGAGGAGGAGGCICCGAIGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 CCATGCTGCATCCAGAGACTCCCTGGCGGGGGGATCTCCTGGCTGTGCTCCTGGCCC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CCGGAGCCCTGAACAGGAAGGAGATTTCTTGCTCCTCCCTGCACAACCGCCTGCGCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GCTGGGTCCAGCCCCCTGCGGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCC 360
                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                    13.8%; Score 259; DB 13; Length 500;
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8.3e-77;
0; Mismatches 2; Indels
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/db_xref="taxon:9606"
                                                                                       /clone_lib="NIH_MGC_116"
/lab_host="DH10B"
High quality sequence stop: 480.
                                                                            /clone="IMAGE:5183898"
                   Location/Qualifiers
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359; Conservative
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/clone_lib="NIH_MGC_lib"
/lab_host="Ungan: pooled colon, kidney, stomach; Vector:
/lab_host="Dign: pooled colon, kidney, stomach; Vector:
pcMv-SPORT6; Site_l: Not!; Site_l: EcoRy (destroyed); RNA
female, 71 yo male colon; 46 yo male kidney, and pool of
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRy site is
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
023. Note: this is a NIH_MGC Library."
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                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11456 row: 1 column: 08
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603044615F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184962 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGAAACAAGCCGGGTGGCTGAGCCTGTGCACGGAGCACCTGACGGGCCCAACAGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CCATGCTGCATCCAGAGACCTCCCCTGGCGGGGGGATCTCCTGGCTGTGCTCGTGGCCC 180
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99.4%; Pred. No. 6.7e-77;
ive 0; Mismatches 2; Indels (
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                     /clone="IMAGE:5182999"
                                                                                                                                          High quality sequence stop: 7
Location/Qualifiers
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BI760121
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 710)

Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666 TACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGT 725
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clone distribution; MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11461 row: n column: 03
High quality sequence stop: 704.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.5%; Score 254; DB 13; Length 710;
nilarity 99.3%; Pred. No. 3.1e-75;
Conservative 0; Mismatches 3; Indels (
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/lab_host="DH10B"
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/clone="IMAGE:5184962"
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RESULT 26

BM924615

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Anote—"Octanon pooled colon, kidney, stomach; Vector: Anote—"Octanon pooled colon, site_1: EcoRV (destroyed): RNA source anonymous pool of 3 colons, age 26 70 male, 49 yo stomache, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 14 kb, destroyed upon cloning). Average insert size 14 kb, enriched for full-length clones and was constructed by Ceruber (Invitrogen). Research Genetics tracking code
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BM924615
AGENCOURT_6767842 NIH_MGC_116 Homo saplens cDNA clone IMAGE:5761001
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1034)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 CTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGTCCGATGGCCGGAGCCCTGAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 AGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTGGCACCAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 GIGGCIGAGCCAGGCIGIGCACGGAGCACCIGACGGGCCCAACAGACCCAIGCIGCAICC 133
                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 18 http://image.llnl.gov column: 18 high quality sequence stop: 685.
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NIH-MGC http://mgc.ncl.nih.gov/.
Notional institutes of Health, Mammalian Gene Collection (MGC)
Notional institutes of Health, Mammalian Gene Collection (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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023. Note: this is a NIH_MGC Library."
336 c 321 g 189 t 2 others
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Matches 346; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/clone="IMAGE:5761001"
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                                                         5', mRNA sequence.
BM924615
BM924615.1 GI:19374994
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Noticoap http://www.ncbi.nlm.nih.gov/ncicgap.
Notional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
The Substitution of the Toler
Talsaue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NoI-CGAP clone distribution information can be info@inage.lln.gov
Seq primer: -40UP from Gibco.
                                                    EST 10-AUG-2000
                                                  hw29g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3184372 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: Kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP hybridization, this DNA was used as tracer in a subtractive from a pool of 5,000 clones made from the same library (cloneIDs 1323376-1323911, 1456007-1456775, and Fatima Bonaldo.
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 409)
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                                                linear
                                                mRNA
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/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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                                                                          mRNA sequence.
BE552150
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RESULT 27
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be www.bio.llnl.gov/bbrp/image/image.thum/LLNL at:
Insert Length: 1316 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 476.
                                                                                          og71e08.sl NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1591814 3', AA976491.1 GI:3152283
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1795 AGACCCTGTGGGGGAGCGTTCCCTGTGGCATGAACCCCAC 1838
                /clone_lib="NCI_CGAP_Kid6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1591814"
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48 CIGCICITITICACCEGGCCAGACCCTGEGGGCAGCGGAGCTTCCC 1

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δλ g

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/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 1322376-1323911, 1456007-1456775, and 150052-1502855). Subtraction by Bento Soares and M. Fatina Bonaldo.
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                                                                                                                                                                                                        AIS89178 12-MAY-1999
tn48a03.xl NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2171596 3',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1690 TGGGGCCCTTCGCCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGA 1749
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:2171596"
/clone_lib="NCI_CGAP_Kid11"
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High quality sequence stop: 422
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Unpublished (1997)
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AI589178
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/lab_host="Solk (kanamycin resistant)"
/lab_host="Solk (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1:
Bcokl; Site_2: Xhoi; Cloned unidirectionally. Primer:
Oligo di. Pooled kidney tumors 5, adaptor sequence: 5,
GAATTCGGCAGGAG 3, 3, adaptor sequence: 5,
CTCGAGTTTTTTTTTTTTTTTT 3, Average insert size: 1.0 kb."
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CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lednon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 835 Std Error: 0.00
Seq primer: -28ml3 revl Er from Amersham
High quality sequence stop: 256.
High quality consortium/Llone at the consortium and the consortium
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                                                                                                                                                                                                                                           AAJ82202 288 bp mRNA linear EST 26-SEP-1997
nn48f01.rl NCI_CGAP_Kid6 Homo sapiens CDNA clone IMAGE:1087129 5',
mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Length 288;
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/clone_lib="NCI_CGAP_Kid6"
/sex="mixed"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AI657201/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                             information can be
                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 10.7%; Score 200; DB 9; Length 330; al Similarity 99.3%; Pred. No. 5.9e-57; 300; Conservative 0; Mismatches 2; Indels
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High quality sequence stop: 254.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1391955"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                                                                                                                               AA812725.1 GI:2882789
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                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
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                                                                                                                 mRNA sequence.
AA812725
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/clone_lib="NCI_CGAP_GGG"
/clone_lib="NCI_CGAP_GGG"
/tissue_LYpe="pooled germ cell tumors"
/tissue_LYpe="pooled germ cell tumors"
/lab_host="Dath08"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polytimker; Site_l: Not I; Site_2: ECO RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
from the normalized library NCI_CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470993, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
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244 CCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCA 185
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www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 942 Std Error: 0.00
Seq primer: -400P from glbco
High quality sequence stop: 287.
Location/Qualifiers
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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282 CTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCGGCTGACA 327
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BI762690
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                                                                                                                                                                                                                                                                                                                                                                                                               BI517774 928 bp mRNA linear EST 29-AUG-200 603042018F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5182397 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM11455 row: c column: 06
High quality sequence stop: 860.
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                                                                                 0; Gaps
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1 (bases 1 to 928)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Life Technologies, Inc.
cDN Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5182397"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Best Local Similarity
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BI517774
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603048444F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5188643 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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243 GGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGACTGCAGCCTGGCCCA 300
                                                                                                                               Match 9.3%; Score 175; DB 13; Length 852; Local Similarity 99.6%; Pred. No. 7.3e-49;
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/db_xref="taxon:9606"
/clone="IMAGE:5188643"
/clone=lib="NHH_MGC_116"
/lab_host="DH108"
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human.
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AA527105
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AL040183
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                                                                                                      B1757380
603029310F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5199674 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: Drain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NH_MGC Library."
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                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I thoses: 1 to 939)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMI1500 row: c column: 03
High quality sequence stop: 778.
Location/Qualifiers
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417 CTGCACAACGCCTGGCCAGGTGGGTCCAGCCCCTGCGGGTGACA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:5199674"
/clone_lib="NIH_MGC_114"
/lab_host="DH108"
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BI757380.1 GI:15748958
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les 258; Conservative
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                                                                                                                                       mRNA sequence.
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                                                                                                                      DEFINITION
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                                                                    RESULT 35
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CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
www-bio.lnl, gov/bbrp/image/rimage.html
Insert Length: 366 Std Errer: 0.00
Seq primer: -40ml3 fwd. Erf from Amersham
High quality sequence stop: 218.
Location/Qualifiers
              EST 13-NOV-1997
AA527105 274 bp mRNA linear EST 13-NOV-199:
n126e10.s1 NCI_CGAP_Ew1 Homo sapiens CDNA clone IMAGE:971466, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pAMP10; mRNA made from Ewing's sarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research
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DEFINITION DKFZP434F2413_r1 434 (synonym: htes3) Homo sapiens cDNA clone
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 274)
                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1671 AGTGAGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTGATTGGGAAGATGGGCTTCA 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1731 ATTAGATGGCGAAGGAGGACACCGCCAGTGGTCCAAAAAGGCTGGTCTTCCACCTG 1790
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99.5%; Pred. No. 1.6e-38;
tive 0; Mismatches 1; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:971466"
/clone_lib="NCI_CGAP_EW1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
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                                                                                                           AA527105.1 GI:2269174
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Unpublished (1997)
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us-09-944-896-49.oli10.rst

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Washington University School of Medicine
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qk32g01.xl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1870704 3',
                                                                                                                                                                                                                                                                                 This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (PRFZ); Emails s.wiemane@dkfz^heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the CDNA sequencing consortium of the German
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 229)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( pases 1 to 704)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                        This clone (DKFZp434F2413) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 TGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGGAGTGCTCG 959
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207 c 207 g 139 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="DKF2p434F2413"
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/tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.7%; Score 145; DB 9; I
100.0%; Pred. No. 8.9e-39;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
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DKFZp434F2413 5', mRNA sequence.
AL040183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                            sequence also available.
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                                          AL040183.1 GI:5409148
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Unpublished (1997)
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/organism="Homo sapiens"
//organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:1870704"
/clone=lib="NcI_GAP_Kid3"
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/lab_host="DH108"
/note="Corgan: kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I: Oligo(dT) pTrimer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llhl.gov/bbrp/Amage/Amage.html
Insert Length: 310 Std Error: 0.00
Seq primer: -400P from Gibco.
Seq primer: -400P from Gibco.
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/Jab_Dost="DH10B (ampicillin resistant)"
//Jab_Dost="DH10B (ampicillin resistant)"
//Jab_Dost="DH10B (ampicillin resistant)"
//Jab_Dost="DH10B (ampicillin resistant)"
//Jab_Dost="DH10B (ampicillin resistant) (also and resistant resistan
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603043013F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183330 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 698 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1359 GGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCACCTGCCTTCAACTGGAACGACCAGCGC 1418
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 123; DB 14; Length 411; 100.0%; Pred. No. 2.9e-31; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GDB:1271568"
/db_xref="taxon:9606"
/clone="IMAGE:346193"
/clone_lib="Soares_fetal_heart_NbHH19W"
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                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="unknown"
/dev_stage="19 weeks"
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314 286 1810
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BI759353
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/note="Organ: Doled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon: 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length, clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MCC Library."
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 457)

NIH-MGC http://mgc.nci.nlb.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mall.nlb.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1464 row: a column: 04
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603045609F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185803 5',
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found through the I.M.A.G.E. Consortium/LENL at: http://image.llnl.gov
Plate: LLAM11457 row: j column: 03
High quality sequence stop: 723.
Location/Qualifiers
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/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Location/Qualifiers
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Best Local 9
                                                                                                                           source
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us-09-944-896-49.olil0.rst

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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lmage/Amage.html
Insert Length: 519 Std Error: 0.00
Seq primer: -400P from Gibco.
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/clone="lnAGE:2138136"

/clone=lib="NLIGAP_Kid11"

/lab_host="DHIOB"

/note="Yorgan: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker: site_1: Not I; Site_2: Eco RI;

plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI522123 425 bp mRNA linear EST 13-APR-1999 ti78e01.x1 NCI_CGAP_Kidl1 Homo sapiens cDNA clone IMAGE:2138136 3',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AGAAACAAGCCGGGTGGCTGAGCCTGTGCACGGAGCACCTGACGGCCCCAACAGAC 120
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                /clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/clone="IMAGE:5185803"
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A1522123
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Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 130 c 127 g 115 t
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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 150052-150855). Subtraction by Bento Soares and M. Fatima Bonaldo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1742 AAGGAGAAGACCCCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCCT 1801
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 97; DB 9; Louis Pred. No. 1.4e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                             / Match 5.2%; Score 97; DB Local Similarity 100.0%; Pred. No. 1.4 les 97; Conservative 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1752556"
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                                                                                                                                                                                                                                                                Fatima Bonaldo
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Gapbs.remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be http://image.linl.gov
Plate: LLAM9486 row: i column: 19
High quality sequence stop: 721.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        1422 AAAACCCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCA 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                 1482 GGGICCIGAGGCCIGACCACAIGGCICCCICGCCIGGGAGCACCACCGGCICIGCIIA 1541
                                                                                                                                                                                                                        1542 CCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAA 1601
                                                                                                                                                                      /db_xxef="taxon:9606"
/clone="IMAGE:4178394"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss.
                                                                                              0; Gaps
                                                                                                                                                                                                                                             0; Gaps
Query Match 5.1%; Score 95; DB 9; Length 460; Best Local Similarity 99.0%; Pred. No. 6.2e-22; Matches 195; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%; Score 73; DB 12; Length 756; 100.0%; Pred. No. 1e-14; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5', mRNA sequence.
BF527554
BF527554.1 GI:11614917
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                                                                                                                                                                                                                                                                                                                      280 GAGGTCTCAGACCTTGC 264
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COMMENT
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1679 TTAGAAGAAGCTG 1691

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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 538 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 229.
                                                                                                                     A1942280 264 bp mRNA linear EST 08-MAR-2000 wo79a05.x1 NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2461520 3'',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thote="Organ: Kidney; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive from a pool of 5,000 clones made from the same library (CloneDS 132376-1323911, 1456007-1456775, and Forling Pool of 5,000 clones made from the same library (150052-150855). Subtraction by Bento Soares and M.
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                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 264)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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322458 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG608968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2461520"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"/db_xref="taxon:9606"
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Unpublished (1997)
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658 TTAGAAGAAGCTG 670
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                                                                                                                                                                 mRNA sequence.
A1942280
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Best Local Similarity
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us-09-944-896-49.oli10.rst

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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
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Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A.J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett, G.L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 05-FEB-2002
v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 125 c 122 g 85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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BM481198
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1135 AGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTA 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
                                                                                                                                                                                                          /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
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/lab_host="DH10B"
                                                                                                                   Plate: 78 row: B column: 9 Seq primer: ATTTAGGTGACACTATAG.
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                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (Dases 1 to 339)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                   Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
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Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4399
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/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG.
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Plate: 97 row: P column: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDN Library Preparation: M. Bento Soares, Ph.D.
CDN Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
www-bio.lningov/bbrp/image.html
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and Fatima Bonaldo.
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I (bases 1 to 241)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Library made from pooled tissue from day 20 and day 40
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/db_xref="taxon:960g"
/clone="IndexE:2284660"
/clone_lib="NCI_GAP_Kidll"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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a 72 c
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BI518200/c

RESULT 50

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603042018T1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182397 3', BI518200
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                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 911)
NIH-MGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1455 row: c column: 06
High quality sequence start: 37
High quality sequence stop: 202.
Location/Qualifiers
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ive 0; Mismatches 0; Indels
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Tissue Procurement: Life Technologies, Inc.
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Contact: Robert Strausberg, Ph.D.
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December 28, 2002, 15:41:47; Search time 4786 Seconds (without alignments)
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1341)

Rato, S. and Kimura, T.
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Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER
Location/Qualifiers
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HOMO Sapiens mRNA; cDNA DKFZp686E1934 (from clone DKFZp686E1934).
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B., Amid, C. and
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/clone="taxon:9606"
/tissue_type="cDNA-collection"
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/dev_stage="adult" + SfilB"
3171. .3176
(DKFZp686E1934) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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                                                                                                                                                                                                                                                                                        52.3%; Score 981.6; DB 9;
98.6%; Pred. No. 4.4e-204;
live 0; Mismatches 14;
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R. Sitel: Drail (CACTOTGTG)
R. Sitel: Drail (CACTOTGTG)
R. Sitel: Drail (CACTOTGTG)
R. Sitel: Drail (CACTOTGTG)
R. Sitel: Drail (CACCATOTGT)
Description: lst strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments 41.5kb.The Sfil and size selection was performed to the distinct Drail sites of pMELBS-FL3. XhoI sites just outside the constructed by oligo-capping method
(Sugano et al., , Institute of Medical Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
(bases 1 to 2900)

Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
Submitted (17-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                 900
                                                                                                        911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K. Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB060195 2900 bp mRNA linear PRI 13-JT
Macaca fascicularis brain cDNA clone:QccE-21387, full insert
792 AGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC
                                                     781 ATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG
                                                                                  912 GACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACT
                                                                                                                                                              841 GACGICICAACAICAGCACCIGCCACIGCCACIGICCCCCTGGCTACACGGGCAGAIACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligo capping; fis (full insert sequence).
Macaca fascicularis adult male cerebellum cortex cDNA to miclone_lib:macaque brain cDNA library QccE clone:QccE-21387
Macaca fascicularis
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/clone_lib="macaque brain cDNA library QccE"
/dev_staqe="adult"
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//organism="Macaca fascicularis"
/db.xref="taxon.9541"
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end primer [CGACCTGCAGCTCGAGCACA] ).
Location/Qualifiers
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1 (sites)
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igcgrhicsadoaaibaycayspermeyogyrshaagecarnatchy
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Pred. No. 1.7e-143;
0; Mismatches 46; Indels 157;
                      /product="hypothetical protein"
/protein_id="BAB41141.1"
/db_xref="GI:13676427"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compositions and methods for the therapy and diagnosis of ovarian
                                                                                                                                                                        240
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781 GIGGCAGCATCCIACTGGGCTGTCCCAGAAGCCCCGACCCTCAGCACCCAGGGAGGCTCC 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham,J.L., King,G.E., Algate,P.A., Fling,S.P., Retter,M.W Fanger,G.R., Reed,S.G., Vedvick,T.S., Carter,D., Hill,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 TGGGCTGTGGGCGCCCTGTGCTCTGCAGGCCAGACGCGATAGAAGCCTTTGTCTGTG
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                                                                                                                                                         CCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCA
                                                              841 TGCCCGGCCTGCTGGGAGAGACCCTTTTCTCGGAGTCCCCTCCTCTCTGACCAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 others
                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.9%; Score 672.8; DB 6; ilarity 99.3%; Pred. No. 1.5e-136; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 0206317-A 321 24-JAN-2002
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Sequence 321 from Patent W00206317.
AX366554
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/db_xref="taxon:9606"
197 c 212 g 133
                                                                                                                                                                                                                                                                                                                                                                                             690 bp
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Location/Qualifiers
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SOURCE
ORGANISM
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Gaps

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/translation="RVRGCDAPPCCRNPGPWRLPADGKGVLRAWSPERGQLLTPFPGK
GPGREHMGAASAGKRGQKGSWQQTPGSEWANLDYPGPGLTYKTAKDSFRWATGEHQAF
TSFAFGQPATHGFGNCVELQASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS"
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Homo sapiens chromosome 16 clone RP11-252A24, complete sequence.
AC009053
/tissue_type="Brain, anaplastic oligodendroglioma with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1236 GGGCTCACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCC 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1656 CAGTGAGGCCCAGGGAGTGAGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGTTTTGATTG 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1356 ATGGGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCATTCAACTGGAACGACCAG 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1336 TGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATAGCCTCATG 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1716 GGAAGATGGGCTTCAATTAGATGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCT 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1776 GCTCTCTTCCACCTGGCCCAGACCCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCC 1835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 ---GGGTTTGGCAACTGCGTGGAGCTGCAGCTTCAGCTGCATCAACTGGAACGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639 CAGTGAGGGCCAGGGAGTGAGTTAGAAQAAGCTGGGGCCCTTGGCTTTGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1476 GGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519 TGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGATCACATGCCTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                699 GGAAGATGGGCTTCAATGATGAACCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCT
                                                                                                                                                                             /product="Unknown (protein for IMAGE:4178394)"
/protein_id="AaH08616.1"
/db_xref="GI:14250369"
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 550; DB 9; Length 1328; Pred. No. 9.9e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                        244 t
                             ip/19q loss"
/clone_lib="NCI_CGAP_Brn67"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                        /note="Vector: pCMV-SPORT6"
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                                                                                                                                                          /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                  29.3%;
94.1%;
                                                                                                                                                                                                                                                                                                                                     381 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 593; Conservative
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Best Local Similarity
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1328)
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-MAY-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                          TCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA 1023
                                                                                                                                                                                                             CCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTATT 1083
                                                                                                                                                                                                                                                                                                                1084 ACAG-AGCCAGGATGAAATGTCAGAGGAAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1142
                                                                                                                                                                                                                                                                                                                                                                                                                  1143 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1203 GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC 1262
                                                                                                                                  421 CCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTATT 480
                                                                                                                                                                                                                                                                                                                                                                481 ACAGAAGCCAGGATGAAATGTCAGAGGAATGGCGGGGGTGCTGGCCCAGATCAAGAGCCAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                          904 AAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCG 963
                                                  AAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                        DCUUGOLD 1328 bp MRNA linear PI
HOMO Sapiens, clone IMAGE:4178394, MRNA, partial cds.
BC008616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:4178394"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REMARK COMMENT

REFERENCE

DEFINITION

RESULT 6 BC008616 LOCUS

ACCESSION

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PRI 27-JUL-2001

source

FEATURES

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                                                                                                                                            Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                          Direct Submission

Submitted (27-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell

Brive, Walnut Creek, CA 94598, USA
On Jul 27, 2001 this sequence version replaced gi:9256116.

Draft Sequence Produced by DOE Joint Genome Institute
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 16342?)

DOB Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Length 163427;
                                                                                                                                                                                                                                                                                                              www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
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                                                                                                                                                                                                                                                                                                                                                          Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.3. STS Content:
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2.4e-80;
9;
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a 38913 c 40421 g 42501 t
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/organism="Homo sapiens"
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/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                              2 (bases 1 to 163427)
DOE Joint Genome Institute.
                                                                            Direct Submission
Unpublished
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SHGC-32146 G27136
SHGC-36058 G30050.
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PRI 28-FEB-2002
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 177479)

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 28, 2002 this sequence version replaced gi:18071320. Draft Sequence Produced by DOE Joint Genome Institute
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      QY
      1557
      GTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTT
      1616

      Db
      144349
      GTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTT
      144408

      QY
      1617
      GCACAATGCCAGAGTTGGGCAGAGAGGCAGGGCCAGTGAGGCCAGGGAGTCAG
      1676

      DD
      144409
      GCACAATGCCAGAAGTTGGGCAGAGAGGCAGGGAGGCCAGTGAGGCCAGGGCCAGGGAGTCAG
      144468

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        AC009153 177479 bp DNA linear PRI 28-FBB-
Homo sapiens chromosome 16 clone RP11-572F4, complete sequence.
AC009153
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Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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47108 a 39618 c 40894 g 49859 t
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/organism="Homo sapiens"
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DOE Joint Genome Institute.
Direct Submission
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RESULT 8
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Consensus quality: 191546 bases at least Q40
Consensus quality: 193703 bases at least Q30
Consensus quality: 19440 bases at least Q20
Estimated insert size: 0; null estimation
Estimated insert size: 196560; sum-of-contigs estimation
Quality coverage: 2.1474836E7 in Q20 bases; null estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
                                                                              Db 144529 TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTTCCACCTGGCCCAG 144588
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Homo sapiens chromosome 16 clone RP11-396D24, *** SEQUENCING IN
PROGRESS ***, 10 unordered pieces.
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1700: gap of unknown length
3566: gap of unknown length
3566: gap of unknown length
5709: contig of 2143 bp in length
7800: gap of unknown length
7800: contig of 1991 bp in length
14727: contig of 6827 bp in length
14827: gap of unknown length
14827: gap of unknown length
14827: gap of unknown length
16827: contig of 12049 bp in length
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Center Project Name: 558525
Center clone name: RPCI-11_396D24
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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DOE Joint Genome Institute.
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AC126771.1 GI:21717140
HTG; HTGS_PHASE1.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 134948 ACCACATGGCTCCCTCGCCTGCCCTGGCACCGCTCTGCTTACCTGTCTGCTGTCTTACCT 135007
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                       1437 TACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCTG 1496
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Homo sapiens chromosome 16 clone RP11-419C5, complete sequence.
ACO26468
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                                                                                                                                                                                                                                                                                  Length 197460;
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93612: contig of 23383 bp in length 93712: gap of unknown length 197460: contig of 103748 bp in length.
                                                                                                                                                                                                /clone_lib="RPCI human BAC library 11"
47482 c 47491 g 51562 t 900 others
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                                                                                                                                                                                                                                                                                  Score 414.6; DB 2;
Pred. No. 2.3e-80;
0; Mismatches 9;
                                                              Location/Qualifiers
1. 197460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 179675)
DOE Joint Genome Institute.
Direct Submission
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Mammalia, Eutheria, Primates,
1 (bases 1 to 179675)
                                                                                                                                                                         /clone="RP11-396D24"
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                                                                                                                                                                                                                                                                                  Query Match 22.1%;
Best Local Similarity 97.9%;
Matches 420; Conservative C
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Direct Submission

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AC009022.9 GI:18581696
                                                                        Homo sapiens.
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                                94598, USA
Submitted (02-NOV-2001) Production Sequencing Facility, DOE Joint
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DEFINITION Homo sapiens chromosome 16 clone RP11-106J23, complete sequence.
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                    Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 179675;
                                                                                                       estimates computed by the phrap assembly program.
All manually edited bases have been reduced to quality
Quality levels boye 40 are expected to have less than
1 error in 10,000 bp.
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/clone="RP11-419C5"
43464 c 41958 g 44686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
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DoE Joint Genome Institute.

Doe Joint Genome Institute.

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute.
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Submitted (07-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Peb 7, 2002 this sequence version replaced gi:16924076.
Sequence Quality Assessment:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN-1 file.
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
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                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 190595)
DOE Joint Genome Institute.
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91050. .91410
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1. .190595
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Homo sapiens chromosome 16 clone RP11-296110, complete sequence.
AC009060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOF Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 180596)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 4, 2000 this sequence version replaced gi:9256118.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                 Db 179398 TGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAG 179339
                                                                                                                                                                                2y 1797 ACCCTGTGGGGCAGCCGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAA 1856
Db 179338 ACCCTGTGGGGCAGCGAGCCTTCCCTGTGGCATGAACCCCACAGGGTATTAAAATTATGAA 179279
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
                              Db 179458 TGTTAGAAGAAGCTGGGGCCCTTCGCCTTTTGATTGGGAAGATGGGCTTCAATTAGA 179399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 87744 TICTGCTTCCTTCCAGCCAGGAGCACATCTCCCGGTGGGGCCCCAGGGTCCTGAGGCCTG 87803
1677 TGTTAGAAGAAGCTGGGCCCTTCGCCTGCTTTTGATTGGCAAGATGGCCTTCAATTAGA 1736
                                                                                         1737 TGGCGAAGGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAG 1796
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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/db_xref="taxon:9606"
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/clone="RP11-296110"
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DOE Joint Genome Institute.
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WI-16981 G21928
WI-9564 G06056.
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TITLE
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JOURNAL
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AUTHORS
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Pan troglodytes.

Pan troglodytes.

Pan troglodytes.

Eukaryots Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

(bases 1 to 191109)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Barbaria, J., Benton, J., Bimage, M. Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Cartor, T., Chowdiry, I., Chacko, J., Chavez, D., Chen, G., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C. Escotto, M., Falls, T., Ferraguto, D., Flag, N., Ford, J., Garza, N., Gall, R., Gorrell, J.H., Guevara, W., Guneartne, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawe, J., Horlins, B., Hemsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jouloway, C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Laud, B., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lucier, R., Lucier, R., Liu, M., Li, S., Mayliney, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martine, R., Martin, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACUS/265 Pan troglodytes clone RP43-119N13, WORKING DRAFT SEQUENCE, 4
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
Pan troglodytes.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Assembly program: Phrap; version 0.990329
Consensus quality: 191814 bases at least Q40
Consensus quality: 193054 bases at least Q30
Consensus quality: 194113 bases at least Q20
Estimated insert size: 193275; sum-of-contigs estimation
Quality coverage: 0.x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                       Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On OCT 23, 2001 this sequence version replaced gi:16258969.
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54202 ACCACATGGCTCCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCT 54143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180970: contig of 8339 bp in length
181070: gap of unknown length
191108: contig of 10038 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 409.8; DB 2 Pred. No. 2.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid; M77789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: ZUAR
Center clone name: RP43-119N13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9598"
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Worley, K.C.
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97.2%;
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Alborooks, S. L., Adams, C. Adio-Oddola, B., Ali-Osman, F. Allen, C., Adio-Oddola, B., Ali-Osman, F. M., Adams, C., Adio-Oddola, B., Ali-Osman, F. M., Burbaria, J., Benton, J., Elmage, K., Blankenburg, K., Bondin, D., Bouck, J., Buhay, C., Benton, J., Elmage, K., Blankenburg, K., Bondin, D., Buday, C., Bouck, J., Buday, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Charcon, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Carter, M., Duddry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., Chacko, J., Chavez, D., Chan, G., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., David, M. L., Davis, C., David, M. Falls, T., Peraguto, D., Flagg, N., Ford, J., Poster, P., Frantz, P., Garla, J., Rerasque, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garla, J., Garca, N., Gall, R., Garnell, J., Garca, N., Gall, R., Garnell, J., Garca, M., Gall, R., Garnell, J., Garca, N., Garla, A., Garner, T., Garca, N., Gall, R., Gorrell, J., Garca, M., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Hart, M., Havlak, P., Hawes, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Louler, R., Lude, F., Luna, R., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martina, R., Martin, R., Martin, R., Martina, R., Martin, R., Martin, R., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martina, R., Pare, J., Perez, L., Pickers, R., Primus, E., Put, L., Oguls, M., Okwuonu, G., Oragunye, N., Ockedo, R., Pace, A., Paylor, R., Stoch, H., Shutch, M., Shooshtari, N., Seson, I., Sodergran, R., Savery, G., Scher, A., Sherk, A., Stankson, L., Sherk, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, S., Tang, C., Taylor, C., Matlington, S., Wallingson, N., Wallingson, N., Wallin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                           54142 GTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTT 54083
                                                              54022 IGTTAGAAGAAGCTGGGGCCCTTCGCCTTTTGATTGGGAAGATGGGCTTCAATTAGA 53963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1797 ACCCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAA 1856
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Pan troglodytes clone RP43-35B16, WORKING DRAFT SEQUENCE, 8
UNDCAGEGED PIECES.
                                                                                                                                                                                                              TGTTAGAAGAAGCTGGGGCCCCTTCGCCTTTTTGATTGGGAAGATGGGCTTCAATTAGA
                                                                                                                                                                                                                                                                                                                                                          TGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTTCCACCTGGCCCAG
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HTG; HTGS_PHASE1; HTGS_EVLLTOP.
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Pan troglodytes
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AC097271
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KEYWORDS
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us-09-944-896-49.rge

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                             Sequenciny Statistics
Sequenciny vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 202604 bases at least Q40
Consensus quality: 204032 bases at least Q20
Consensus quality: 205164 bases at least Q20
Estimated insert size: 200244; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarcse-fp estimation
Quality coverage: 9.4x in Q20 bases; sum-of-contigs estimation
Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48992: contig of 48992 bp in length 49092: gap of unknown length 90442: contig of 41350 bp in length 90542: gap of unknown length 124888: contig of 34346 bp in length 145488: gap of unknown length 145269: contig of 20281 bp in length 145369: gap of unknown length 173261: contig of 20281 bp in length 173361: contig of 13171 bp in length 186532: contig of 13171 bp in length 186532: contig of 15040 bp in length 201672: contig of 15040 bp in length 201772: gap of unknown length 201772: gap of unknown length 201772: gap of unknown length 201772: contig of 15040 bp in length 201722: gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
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50970 c 50521 g 49254 t
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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                       Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: RP43-35B16
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                                                                    JOURNAL
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                                                                                                REFERENCE
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HTG 22-JUN-2002
         17350 GTCTGGAACAAGGTTCCACCTGTCTGGAACAAGGTTAAGACCACATGCCTCATGTCCAAA 17409
                                                                                                                                   17530 TGGGCTTCAATTAGATGCCGAAGGAGGACCCCGCCAGTGGTCCAAAAAGGCTGCTCTC 17589
                                                                                                                                                                                    17590 TTCCACCTGGCCCAGACCCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACAGG 17649
                                                          17410 GAGGTCTCAGACCTTGCACAATGCCAGAAGTTGGGCAGGAGGAGGCAGGGAGGCCAGCGA 17469
                                                                                                    17470 GGGCCAGGGAGTGAGTGTTAGAAGATGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGA 17529
--GCCAGGTTAAGACCACATGCCTCATGTCCAAA 1601
                                        TGGGCTTCAATTAGATGGCGAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTC 1781
                                                                                                                                                                 TTCCACCTGGCCCAGACCCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACGGG 1841
                                                                                                                                                                                                                                                                      GGGCCAGGGAGTGAGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGA
                                                                                          AC097331.4 GI:21535856
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
chimpanzee.
                                                                                                                                                                                                                              Db 17650 GTATTAAATTATGAATCAGCTGAA 17673
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 GTCTGGAACAAGG---
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AC097331/c
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                                                                                                                                                                                                                                                                                                              ACCESSION
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KEYWORDS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; M77789
Consensus quality: 1987810 bases at least Q40
Consensus quality: 193098 bases at least Q30
Consensus quality: 193098 bases at least Q30
Estimated insert size: 2128111; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; sqarose-fp estimation Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation
Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wand'Moner, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., T., Zhou, J., Zorrilla, S., Nelson, D., Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (22-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 21, 2002 this sequence version replaced gi:21450389.
                                                                                                                                                                                                                                                                                                           Submitted (14-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 200409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39411: contig of 39411 bp in length 612029; gap of unknown length 62029; gap of unknown length 62029; gap of unknown length 87446; contig of 22418 bp in length 87546; gap of unknown length 113623; contig of 26077 bp in length 113723; gap of unknown length 130748; contig of 17025 bp in length 130848; gap of unknown length 142400; contig of 1752 bp in length 142500; contig of 14250 bp in length 156850; gap of unknown length 156850; gap of unknown length 169557; contig of 12707 bp in length 169557; gap of unknown length 1695400; contig of 10083 bp in length 169400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 11898 bp in length
unknown length
of 2153 bp in length
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of 2047 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: hgsc-help@bcm.fmc.edu
------ Project Information
Center project name: ZAA2
Center clone name: RP43-53A2
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contig
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Worley, K.C.
Direct Submission
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AUTHORS
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TITLE
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Qy 1662 GGGCCAGGGAGTGATTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGA 1721
Db 128132 GGGCCAGGGAGTGATTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGA 128073
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 128372 TTCTGCTTCCTTCCAGCCCAGGAGCACATCTCCCTGTGGGGCCTAGGGTCCTGAGGCCTG 128313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 128312 ACCACATGCCTCCCTCGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCCCCCT 128253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 128072 TGGGCTTCAATTAGATGCCGAAGAGAGGACCCGCCAGTGGTCCAAAAAGGCTGCTCT 128013
                                                                                                                                                                                                                                                                                                                                                                                                                             QY 1437 TACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTG 1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY 1497 ACCACATGGCTCCCTCGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCT 1556
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                                                                                                                                                                                                                                                                                                                    Query Match 19.9%; Score 373.6; DB 2; Length 200409; Best Local Similarity 92.3%; Pred. No. 2.1e-71; Matches 410; Conservative 0; Mismatches 19; Indels 15;
                                                                                                                                                                                                      /clone="RP43-53A2"
55207 a 46732 c 45615 g 51554 t 1301 others
196238: gap of unknown length
198281: contig of 2043 bp in length
198381: gap of unknown length
200409: contig of 2028 bp in length.
                                                                                                                                                          /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 28, 2002, 19:54:31 Job time : 6359 secs
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                                                                                                           Location/Qualifiers
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ORIGIN
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Sequence 18, Appl
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Sequence 17, Appl
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                                                                                          (without alignments)
7664.697 Million cell updates/sec
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                                                                                                                                                        1 atgctgcatccagagacctc......gaaaccgttacatctgccag 1326
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Sequence 98,
                                                                            December 28, 2002, 16:48:37; Search time 53.0554 Seconds
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                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_NA:*

'Gqn2_6/ptodata/2/ina/5A_COMB.seq:*

'Gqn2_6/ptodata/2/ina/5B_COMB.seq:*

'Gqn2_6/ptodata/2/ina/6A_COMB.seq:*

'Gqn2_6/ptodata/2/ina/BE_COMB.seq:*

'Gqn2_6/ptodata/2/ina/PCTUS.COMB.seq:*

'Gqn2_6/ptodata/2/ina/PCTUS.COMB.seq:*

'Gqn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-387-942C-18
US-08-387-942C-1
US-08-3747-1
US-08-404-655-3
US-08-404-671-3
US-08-404-671-3
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US-08-485-618-98
US-08-605-672-98
US-08-482-293A-98
US-08-943-363-98
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US-08-605-672-1
US-08-482-293A-1
US-08-943-363-1
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US-09-387-574-9
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US-08-286-889-1
US-08-485-618-1
                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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US-09-470-443-7
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                                                                                                                                                                                                                           441362 seqs, 153338381 residues
                                                                                                                                  US-09-944-896-49_COPY_123_1448
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                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.462C2
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 Sequence
                              Sequence
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Pred. No. 5.9e-153;
0; Mismatches 4;
US-09-193-043-98
US-09-688-307A-98
US-08-485-618-97
US-08-482-293A-97
US-08-943-363-97
US-09-193-043-97
US-09-193-043-97
US-09-257-583-12
US-09-074-912-3
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US-09-073-368-2
US-09-073-368-2
US-09-074-912-3
US-09-073-368-2
US-09-199-887-2
                                                                                                                                            US-09-471-396-2
US-09-105-537-30
US-09-105-537-5
US-09-320-878-19
                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEO ID NOS: 393
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                          Sequence 321, Application US/09404879A Patent No. 6468546
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(690)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-321
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Matches 685; Conservative
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36778
38506
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748
1227
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970
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
    RESULT 1
US-09-404-879A-321
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LENGIH: 690
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962 ACAG-AGCCAGGATGAAATGTCAGAGGAAAGGCGGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
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842 TCTGTGACATCGGCTACGGGGGGGGGCCCAGTGTGCCAAGGTGCATTTTCCCTTCCACA 901
                                                       902 CCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTATT 961
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famedu, Omolayo O.
APPLICANT: Famedu, Omolayo O.
APPLICANT: Han, Feng
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Disease Resistance Factors
FILE REFERENCE: BB125 US NA
CURRENT APPLICATION NUMBER: US/09/433,248A
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,242
PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                   1141 TCCTTCCGCTGGGCCACAGGGGAGCACCAG 1170
                                                                                                                                                                                                                                                                                                                  661 TCCTTNCGCTGGGCCACAGGGGAGCACCAG 690
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09433248A Patent No. 6355462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (421)
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(564)
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                                                                                                                                                                                                                                                                                                                                                                                 US-09-433-248A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
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                                                                                                                                          1088 ACTICGAGACCAGGAACTICTGGATCGGGCTCACCTACAAGACCGCCAAGGACTCCTTCC 1147
                                                                                                                                                                                                                             1148 GCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCTGACAACC 1207
                                                                                                                                                                                                                                                                                                                1208 ACGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTGCAGGCTT 1267
                                                                                                                                                                                                                                                                     61 GGCAAGCCATCGGCAGGGACACGTGGAGCGCCATCTTCGGGTGGCTCGCGCGCCCAACG 120
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                   1 ACATCCTGAACCGGACCATGCCATGGACACCTCCAACAAGGCCACCTCCGACTACGTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                       181 GGCGGTTCCCGCACCGCGGCGGCGTGCTCTACAACATCCAGTACATGAACTTCTG 235
                                                                                                                  0
                                                              Score 47.8; DB 4; Length 582;
Pred. No. 0.01;
0; Mismatches 117; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/08387942C
gratent No. 5939289
GRNERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SYBIN
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: BNA COMPOUNDS COMPRISING SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                3.6%;
50.2%;
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                                                                                                    Matches 118; Conservative
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MEDIUM TYPE: Floppy
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                                                                                     Sest Local Similarity
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Matches 110; Conserva
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LOCATION: (571)
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; LOCATION: (5)
US-09-433-248A-3
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                                                                                                                             1014 GAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGA 1073
                                                                                                                                                   357 CGGCTGGTTCAACGGCTACATCCCCGGCCAGGACGCCGCCGATCGCGAGGTGACCCTGGA 416
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: VALLA, SVEIN
APPLICANT: LARSEN, BJORN
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        1074 GGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCG 1114
                                                                                                                                                                                                                            477 CCTGACGATCCGCGACAGCGTGGCCCACGACAGCCTCG 517
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STREET: P.O.BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
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STRAIN: E
                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08387942C
Patent No. 5939289
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NAME: MURPHY JR, GERALD M.
REGIESTRATION NUMBER: 28,977
REFERENCE/COCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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6702..9695
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9973..12588
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LOCATION: 290..1951
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LOCATION:
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FEATURE:
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                                                                                                                                                                                                                 1014 GAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGA 1073
                                                                                                                                                                                                                                      2643 GCGGTGGAAATCCGCGAGATGTCCGGCTACGGTTTCGACCCCCCACGAGCAGAACATCAA 2702
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                                                                     894 CTICCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGA 953
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3.3%; Score 43.4; DB 2; Length 12588; 49.8%; Pred. No. 0.27;
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                                  0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                            2703 CCTGACGAITCGCGACAGCGTGGCCCACGACAACAGCCTCG 2743
                                                                                                                                                                                                                                                                                       1074 GGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCG 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
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Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FF
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TELEFAX: (619) 535-8949
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                 Best_Local Similarity 49.8
Matches 110; Conservative
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112..2848
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; LOCATION:
PCT-US95-03747-1
Query Match
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942 TTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCT 1001
                                                                                             2223 TTCTGCCCGAAGGAGGAGGAGGAGGAGGAACAAQTGCCGGATGTACGGCGCGCACCT 2282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    765 CACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGA 824
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                                                                                                                                                                                                                                                                            Sequence 3, Application US/08404665
Patent No. 5591583
GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and STREET: 1 Becton Drive
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,665
                                                                                                                                                                  2283 GGCCAGCATCAGCACGCGGAGGAACAGGACTTCATC 2319
                                                                                                                                           1002 GGCCCAGATCAAGAGCCAGAAGTGCAGGACATCCTC 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: 9-33.
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4724 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-08-404-671-3
; Sequence 3, Application US/08404671
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Best Local Similarity 52.33
Matches 90; Conservative
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MOLECULE TYPE: CDNA
US-08-404-665-3
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705 CTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTA 764
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Patent No. 5681931

GENERAL INFORMATION:
APPLICANT: Acid, Robert A.
APPLICANT: Hemperly, Shonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: BEQUENCES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Company
STREET: 1 Becton Drive
CITTY: 1 Becton Drive
                              APPLICANT: Reld, Robert A.
APPLICANT: Reld, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John B.
TITLE OF INVENTION: SEQUENCES
NUMBER OF EDUENCES: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/404,671
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-PARA SOFTWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PINFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 4724 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.39
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1 Becton Driv
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
                                                                                                                                                                                                                                                                                                           ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA US-08-404-671-3
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Patent No. 5635360 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              825 GGAGGAGTGCTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCC 876
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Patent No. 593289

GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA

APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: VALLA, SVEIN

TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES

TITLE OF INVENTION: BACODING MANNURONAN C-5-EPIMERASE

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: P.O.BOX 747

COTY: FALLS CHURCH

COTY: FALLS CHURCH

COTY: COTY: FALLS CHURCH

COTY: COTY: FALLS CHURCH
                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/387,942C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: FUGIT, DONNA R.
REGISTRATION NUMBER: 22,135
REFERENCE/DOCKET NUMBER: P-3341
INFORMATION FOR SEQ ID NO: 3:
SQUENCE CHARACTERISTICS:
LENGTH: 4724 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                      APPLICATION NUMBER: US/08/404,78
                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                          FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                    1011 CAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAA 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1071 CGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGAC 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                873 CGACAACGCGCAGGCGGCCGTGCCCGAGGTCCTGCTGCAGTCCTTCGACGATACCGC 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 GCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCLICASIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                             Query Match 3.0%; Score 39.4; DB 2; Length 1176; Best Local Similarity 52.1%; Pred. No. 1.3; Matches 88; Conservative 0; Mismatches 81; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1131 CGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACC 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09103840A Patent No. 629428 Patent No. 629428 APPLICANT: FLEISCHMAN, Robert D.
                                              TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1176 base pairs
TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHITE, Owen R.
                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                         US-08-387-942C-17
                                                                                                                                                                                                               TOPOLOGY:
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US-08-387-942C-21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1014 GAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAAGGA 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   894 CTICCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGA 953
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                                                                                                                                                     TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: PO.80X 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Tony
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Geranylgeranyl Transferases
FILE REPERENCE: BB-1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1074 GGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCG 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.9%; Score 38.6; DB 2; Best Local Similarity 48.4%; Pred. No. 2; Matches 107; Conservative 0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1809-106P
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 21, Application US/08387942C Patent No. 5939289 GENERAL INFORMATION:
                                                                   APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVUEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFRENCE/POCKET NUMBER: 1809
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09387574 Patent No. 6168951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) US-08-387-942C-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-09-387-574-9
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                            CITY: F
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Patent No. 6312954

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Tony
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Geranylgeranyl Transferases
FILE REFERENCE: BB1239 US NA DIV
CURRENT APPLICATION NUMBER: US/09/668,096
CURRENT FILING DATE: 1998-09-01
PRIOR PELLING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/9817,534
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
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Best Local Similarity 51.5%; Pred. No. 4.6;
Matches 86; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                   0; Mismatches
CURRENT APPLICATION NUMBER: US/09/387,574
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: 60/098,743
EARLIER FILING DATE: September 1, 1998
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-470-443-7
; Sequence 7, Application US/09470443
                                                                                                                                                                                                                                                                                              Best Local Similarity 51.5
Matches 86; Conservative
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US-09-668-096-9
                                                                                                                                                                                    TYPE: DNA
CORGANISM: Oryza sativa
US-09-387-574-9
                                                                                                                                          SEQ ID NO 9
LENGTH: 2335
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US-09-668-096-9
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                                 APPLICANT: Lettin, Michael I.
APPLICANT: Lattif, Farida
APPLICANT: Lattif, Farida
APPLICANT: Lattif, Farida
APPLICANT: Sekido, Yoshitaka
APPLICANT: Sekido, Yoshitaka
APPLICANT: Gao, Boning
APPLICANT: Gao, Buning
APPLICANT: Gao, Buning
APPLICANT: Buh, Fuh-Mei
TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
CURRENT APPLICATION NUMBER: US/09/470,443
CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 60/114,359
EARLIER FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 AACGCCACCTGCACCCACTACACGCAGCTCGTGGGGCCACCTCAAGCCAGCTGGGCTGT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     803 CIGIGGCIGCIGCIGCIGCIGCITILIACCGCIGCICCICGCCCCCGGCGCCCTCTGCCTACAGC 862
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APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael

APPLICANT: Van Der Vienen, Monica

TITLE OF INVENTION: Subunit

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: AARSHALL, O'TOOLE, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37.2; DB 4; Length 1 Pred. No. 4.2; 0; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/173,497 FILING DATE:
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Patent No. 5437958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%;
Best Local Similarity 46.0%;
Matches 126; Conservative
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ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Illinois
                        GENERAL INFORMATION:
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US-08-173-497-1
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Patent No.
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2375 CGTGGGGAGCTCCCTGGAGCTCAACGTGATTGTGACTGTGTGGAACGCAGGTGAGGATTC 2434
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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Pred. No. 5.9;
0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 28, 2002, 21:38:49 Job time: 1461.06 secs
                                   NAME: NO. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31363
                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        2.8%;
                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.8%
Best Local Similarity 56.6%
Matches 69; Conservative
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3..3485
                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-173-497-1
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

December 28, 2002, 21:39:38; Search time 4743 Seconds (without alignments) 11511.040 Million cell updates/sec 2077837 1 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: Post-processing: Listing first 1000 summaries OM nucleic - nucleic search, using sw model OLIGO_NUC . / Gapop 60.0 , Gapext 60.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 gb_ba:*
gb_htg:*
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gb_om:*
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gb_ph:*
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Pred. No. is the number of results predicted by chance to have a

em_htgo_mus:*
em_htgo_other:*

em_htg_vrt:* em_sy:* em_htgo_hum:*

em_htg_hum:*
em_htg_inv:*
em_htg_other:*

em_sts:* em_un:*

em_vi:*

em_ro:*

em_htg_mus:* em_htg_pln:* em_htg_rod:* em_htg_mam:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	.;	503 Sequenc	193 Sednenc	554 Sequence	339 HOMO Sap	153 Homo sap	771 Homo sap	168 ношо зар	122 Homo sap	265 Pan trog	060 Homo sap	331 Pan trog	271 Pan trog	125 Homo sap	195 Macaca f	331 Pan tro	125 Homo sap	USI HOMO Sap 951 Homo sar	451 Mus mus	076 Rattus	865 Caulon 331 Human	nuation (2	mi	954 Mus mus	905 ношо s	1488 Mouse 591 Homosa	464 Mus musc	604 Mus mi	302 HOMO :	766 Homo	175 Rhizol 7 Human C	5 Sequence	321 Seque	œα	322 Seque	7	903 Homo	494 Homo	521 Sus s	ŭ, iv	712 Humar	940 Homo	1336 Mus n	1962 Homo sap	AC080148 Homo sap	AC01337	068 Homo sap	556 Rattus	1537 Homo sa	8	141 Mus mus
SUMMARIES DB ID		AX19150	AX19149	AX366554	HSM8046	AC00903	AC12677	AC02646	AC00902	BC00861	AC00906	AC09733	AC09727	AC00912	ACUZISS AROKO19	AC09733	AC00912	AK09605	AC09345	AC0980	AEUUSBB	HSS171M	AC07931	AL80595	AC079905	ALE	AC09346	AC12460	AC09043 HS21C10	BC033766	RLE4311	A47885	AR0	HSU2202	AR06932	AL807743	AC07890	AC01049	AL77352	AL77356	ACULISI AL15771	HS117P2	AC12233	AC01252	AC08014	AC013371	AC02706	AC12555	AC11969	2 AC127524	AC12514
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11 1994 Control Co	AL138479 Human chr AC012507 Homo sapi AC115290 Mus muscu AP002783 Homo sapi AC017001 Homo sapi AC091755 Mus muscu AC091759 Homo sapi	ACU/2042 Homo Sapi AC095307 Rattus no AC008542 Homo Sapi AC069526 Homo Sapi AC104012 Homo Sapi	AC114012 HOMO Sapi AC111655 Rattus no AC127472 Sus scrof	AC096039 Rattus no AC067721 Homo sapi	AC069246 Homo sapi AC069246 Homo sapi	Hum	AC025518 Homo sapi	Sus	Bos	AC113228 Bos tauru AC124478 Mus muscu	AC066589 Homo sapi	AC079823 Homo sapi	AC022206 Homo sapi AL732473 Mus muscu	AC073413 Homo sapi	AL161646 Human DNA	AC087474 Homo sapi	HOMO	Ē Ē.	<u> </u>	AC011669 Homo sapi AC091560 Homo sapi	E C		Į į	ins Hom	ion Tus	AC112258 Mus muscu	AC050124 Kattus no AC067951 Homo sapi	AC003684 Homo sapi	AC124347 Mus muscu	AC012363 Homo sapi	AC112142 Mus muscu AL806527 Mus muscu	Mou	AL844873 Mus muscu AC125523 Mus muscu
1111700000	WS 007 013 59 59	24 07 07 06 01	1.2 7.2 1.0	0 0 1	~ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	2 K	18	55	18	28 78	98	23)6 73	13	9 9	0 4 •	. 0 9	000	88	60	11	2 0		2.2	7	58	† ਜ਼	4.ε. Ε.	7 8	n en e	7.2	26 1	e e
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BC022771 Mus muscu AK093399 Homo sapi MA1477 Rattus norv AR175387 Homo sapi AR177374 Sequence AK025991 Homo sapi BC011100 Mus muscu AY075570 Drosophil BC0110095 Homo sapi AF042080 Homo sapi	AF10787 Homo sapi AF107848 Homo sapi AF107848 Homo sapi M84425 Homo sapien M8425 Homo sapien X14723 Human SP-40 AF202086 Sequence I17171 Sequence 27 AF176527 Mus muscu BC010514 Homo sapi ABC010514 Homo sapi ABC01881 Macaca fa U97144 Homo sapien AF05614 Homo sapien AF05614 Homo sapien AF0296 Human subst AV070956 Drosophil AX283091 Sequence AX283091 Sequence AX283091 Sequence AX283091 Sequence AX283091 Sequence AX283091 Sequence	AK023724 Homo sapi AK023724 Homo sapi AK028194 Sequence AR176410 Sequence AK16569 Sequence AK097494 Homo sapi BC003809 Mus muscu AK11288 Rattus no AK092418 Sequence AK311288 Rattus no AK092418 Sequence AK39254 Sequence BC034854 Mus muscu AX399254 Sequence AL512755 Homo sapi BC003727 Mus muscu AX053103 Sequence AX053103 Sequence	AX083354 Sequence AX399256 Sequence E02020 cDNA encodi E05489 cDNA encodi BC030409 Mus muscu M2852 Rabbit cyto BC011603 Homo sapi
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// LTanslation="MLHPETSPGRGHLLAVLLALLGTAMAEVWPPOLQEQAPMAGALN RKESFLLLSLHNRLRSWVOPPAADMRRLDWSDSLAOLAQARAALCGIPTPSLASGIWR TLQVGWNANGLLPAGLASFVEVSLWFRESGORYSHAAGBCCARNATCHIPTGLWAGASGWNASQULGGWGWNAOLLASFVEXYSLWFRESGORYSHAAGBCCARNATCHITQLWAGASGORHLCSAGQAAIEAFVCAXSPGGRWEWNEXTIIPFKKGAMGSLCTAXSVGGFKRWDHAGGLEVPRNPCRMSCONHGRLNISTCHCHCPPGYTGRYCGOVCIGTARSVGGFKRE ECSCYCDIGGAGCATKVHRPFHTCDLRIDGDFFWSSEADTYYRARMKCQRKGGVLAQIKSQKVODILLAFYLGRLETTNEVIDSDFFFRNFWIGLTYKTAKDSFRWATGEHQAFTSFRAGASAGNANNORCKTRNRYICQFAQEHISRWGPGS"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1775)
Kato,S. and Kimura,T.
                                                                                                                                      Human proteins having hydrophobic domains and dnas encoding these
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                                                                                                                                                                                                      Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
Location/Qualifiers
| Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifi
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TITLE
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PAT 15-AUG-2001

linear

DNA

Sequence 25 from Patent W00149728. AX191503 AX191503.1 GI:15209689

LOCUS DEFINITION

AX191503

ACCESSION VERSION KEYWORDS

Homo sapiens human.

ORGANISM

SOURCE

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1341)
Kato,S. and Kimura,T.
                                                                                                                                                                                                942 CGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACC 1001
                                                                                                                                                                                       AAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTG 1061
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                                                                                                                                                                                                                                                                                                                                                             1242 ACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACC 1301
882 GGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCGCGGCCGGTTC 941
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                                                                  822 ATGAGCTGCCAGAACCATGGACGTCTCAACATCAGGACCTGCCACTGCCACTGTCCCCCT
                            762 IGCTICAAAGCCIGGGACCAIGCAGGGGGGCTCIGTGAGGICCCCAGGAAICCTIGICGC
                                                                                                                   TCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAAGGGGGGTG
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99.7%; Pred. No. 0;
tive 0; Mismatches 4;
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Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY Submitted (09-JUL-2002) 1, D-85764 Neuherberg, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZpG86E1934) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/.
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/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sf1; host
DH10B; sites SfiIA + SfiIB"
                                                                                                     HSMWU4052 3293 bp mRNA linear PRI 10-JUL-2002
HOMO Sapiens mRNA; cDNA DKFZp686E1934 (from clone DKFZp686E1934).
AL833339
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B., Amid, C. and
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0206317-A 321 24-JAN-2002;
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (27-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 27, 2001 this sequence version replaced gi:9256116.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actoratos 163427 bp DNA linear PRI 27-JUL-2. Actorograms chromosome 16 clone RPI1-252A24, complete sequence. ACO09053
                                           GCACCCIGCAAGIGGGCIGGAACAIGCAGCIGCTGCCGCGGGCIIGGCGICCTIIGIIG 486
                                                                                                    487 AAGTGGTCAGCCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      677
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                                                                                                                                                                                                                                               CCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAG 786
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                 547 CTCGCAACGCCACCTGCACCACTACACGCAGCTCGTGTGGGGCCACCTCAAGCCAGGTGG
                                                                                                                                                                                   607 GCTGTGGGCGGCACCTGTGCTGTGCAGGCCAGACAGGGATAGAAGCCTTTGTCTGTGCCT
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Finishing Completed at Stanford Human Genome Center
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DOE Joint Genome Institute.
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AC009053
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PRI 28-FEB-2002
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (05-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                 1452 GCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCT 1511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 16 clone RPI1-572F4, complete sequence.
AC009153
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                       22.1%; Score 414; DB 9; Length 163427; 100.0%; Pred. No. 1.1e-230;
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www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
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/clone="RP11-252A24"
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                                                                                                               Location/Qualifiers
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DOE Joint Genome Institute.
Direct Submission
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                                                             SHGC-32349 G27498
SHGC-32146 G27136
SHGC-36058 G30050.
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                                            STS Content:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 144244 GCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCT 144303
                                                                                 Submitted (28-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Feb 28, 2002 this sequence version replaced gi:18071320. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGGAGGA 1751
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Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 177479)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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100.0%; Pred. No. 1.1e-230;
tive 0; Mismatches 0;
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE1.
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Matches 414; Conservative
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AC126771
                                                  AUTHORS
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Consensus quality: 193703 bases at least 030
Consensus quality: 194840 bases at least 020
Consensus quality: 194840 bases at least 020
Consensus quality: 194840 bases at least 020
Estimated insert size: 196660; sum-of-contigs estimation
Estimated insert size: 196560; sum-of-contigs estimation
Quality coverage: 8.2 in 020 bases; null estimation

* NOTE: This is a "working draft" sequence. It currently
* NOTE: This is a "working draft" sequence record is
* consists of 10 contigs. The true order of the pieces
* arbitrary. Gaps between the contigs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
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DD 134903 GCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCTT 134962
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Direct Submission
Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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197460: contig of 103748 bp in length.
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contig of 1766 bp in length
gap of unknown length
contig of 2143 bp in length
gap of unknown length
contig of 1991 bp in length
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93712: qap of unknown length
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contig of 6827 bp in length
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                                                                                                                                                                                                                                                     Center clone name: RPCI-11_396D24
                                                                                                                                                      Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                            Center: Joint Genome Institute
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/clone="RP11-396D24"
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Direct Submission

Submitted (02-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Nov 2, 2001 this sequence version replaced gi:14589452.

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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DOB Joint Genome Institute.
Sequencing of Human Chromosome 16
                            Db 135203 CACCGCCAGTGGTCCAAAAAGGCTGCTCTTTCCACCTGGCCCAGACCCTGTGGGGCAGC 135262
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                 CACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCCTGTGGGGCAGC 1811
GGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGGAGGA 1751
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                                                                                                                                                                                                                                                                                                                         Db 135263 GGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAATCAGCTGAA 135316
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49567 a 43464 c 41958 g 44686
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DOE Joint Genome Institute.
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AC026468/c
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DB 9; Length 179675;

17.9%; Score 336;

Query Match

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PRI 07-FEB-2002
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DOE Joint Genome Institute.

DIRECT Submission
Submitted (07-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA CON FED 7, 2002 this sequence version replaced gi:16924076.

This entry has been annotated with sequence quality
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 16 clone RP11-106J23, complete sequence.
AC009022
AC009022.9 GI:18581696
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    Pred. No. 7.4e-185;
0; Mismatches 1;
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2 (bases 1 to 190595)
DOE Joint Genome Institute.
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      Best Local Similarity
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AC009022/c
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AC097265/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 179623 GGCCTGGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGC 179564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 179563 CAGGTTAAGATCACATGCCTCATGTCCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAG 179504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 179443 GGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGCCGAAGGAGGA 179384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 179383 CACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCCTGTGGGGGCAGC 179324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                   1452 GCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCT 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1512 CGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGC 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1572 CAGGITAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAG 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1632 TIGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGTGATAGAAGAAGCTG 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1692 GGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGCCTTCAATTAGATGGCGAAGGAGAGA 1751
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                          Length 190595;
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mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                             /clone="RP11-106J23"
91050. .91410
/note="unresolved tandem repeat"
a 43243 c 43697 g 52220 t
                                                                                                                                                                                                                                                                                                                  17.9%; Score 336; DB 9; I ilarity 99.7%; Pred. No. 7.4e-185; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens, clone IMAGE:4178394, BC008616
                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 179323 GGAGCTTCCCTGTGGCATGAACCCCAC 179297
                                                                                                                                                          /db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1812 GGAGCTTCCCTGTGGCATGAACCCCAC 1838
                                                                                                  Location/Qualifiers
1. .190595
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error in 10,000 bp.
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                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                          Matches 386;
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                                                                                                  FEATURES
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/traislation="RYPRGCDAPPCCRNPGPWRLPADGKGVLRAWSPERGQLLTPFPGK
GPGREHMGAASAGKRGGKGSWQQTPGSEWANLDYPGPGLTYKTAKDSFRWATGEHQAF
TSFAFGQPATHGFGNCVELQASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS"
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                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                  Lu, X., Garcia,
J., Yu, W.,
                                                                                                                                                                                                                                                            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 12 Row: h Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Brain, anaplastic oligodendroglioma with 1p/19q loss"
/clone_lib="NCI_CGAP_Brn67"
/lab_host="NH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1419 TGCAAAACCGGAAACGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGC 1478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1539 TTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCC 1598
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DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J.,
Muzny, D.M., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /produ_t="Unknown (protein for IMAGE:4178394)"
/protein_id="AAH08616.1"
/db_xref="G1:14250369"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.2%; Score 323; DB 9; Length 1328; Best Local Similarity 99.7%; Pred. No. 3e-177; Matches 373; Conservative 0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                   1. 1328
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4178394"
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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ORGANISM

KEYWORDS

VERSION

REFERENCE AUTHORS

ACCESSION

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Quality coverage: 0x in Q20 bases; agarose-fp estimation
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                                                                                                                                                                                                                       Mammalia Eutheria; Primates; Catarrhini; Hominidae; Pan.

I (Dases I to 19108)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaretunge, H.C., Are, J.K., Banks, T., Barbaria, J.,
Bentoon, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bentool, S.L., Amaretunge, H.C., Are, J.K., Barks, T., Barbaria, J.,
Bentool, S.L., Amaretunge, H.C., Are, J.K., Bould, B., Bunkett, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Coyle, M.D., Dathorne, S.R., David, R.L., Byrd, N.C.,
Denn, A.L., Ding, Y., Dutpin, H.H., Douthwalte, K.J., Deraper, H.,
Dugn-Recha, S., Dutpin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraquto, D., Flago, N., Ford, J.,
Entraltz, P., Gablsi, A., Gao, J., Garcia, A., Garner, T.,
Bungan-Recha, S., Dutpin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Ealls, T., Ferraquto, D., Flago, N., Ford, J.,
Escotto, M., Gall, K., Garcell, J.H., Guevara, W., Gunarane, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Joudah, S., Karlsson, E., Elly, S., Khan, U., King, L., Korvah, J.,
Joudah, S., Karlsson, E., Elly, S., Khan, U., Karlson, R.,
Martinez, E., Maschiney, E., Martin, R., Martindale, A.,
Martinez, E., Mayen, M., Mapus, P., Martin, R., Martinez, E., Marker, M., Mapus, P., Martin, R., Mahaehwari, M., Mayusen, N., Nickerson, E., Nocker, M., Petch, R., Man, Mayusen, N., Nickerson, E., Wall, Man, Martis, S., Marten, M., Mayusen, N., Suboshka, Man, Tang, H., Tansey, J., Terers, Martington, S., Wall, Man, Man, Ma
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Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 23, 2001 this sequence version replaced 9i:16258969.
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 191814 bases at least 040
Consensus quality: 193054 bases at least 020
Estimated insert size: 193275; sum-of-contigs estimation
                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Web site: http://www.hgsc.bcm.tmc.edu/
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                          AC097265.3 GI:16328241
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unordered pieces.
                                                                                                                  Pan troglodytes.
Pan troglodytes
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TITLE JOURNAL

REFERENCE AUTHORS JOURNAL

TITLE

COMMENT

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)...
NOTE: This is a "working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
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HOMO sapiens chromosome 16 clone RPI1-296110, complete sequence.
ACC009060
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180596)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                               NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                              * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 287; DB 2; Length 191108;
                                                                                                                                                                                                                                                                                                                                                                1 121806: contig of 121806 bp in length 121807 121906: gap of unknown length 172531: contig of 50625 bp in length 172532 172631: gap of unknown length 172632 180970: contig of 8339 bp in length 180971 181070: gap of unknown length 181071 191108: contig of 10038 bp in length.

        QY
        1692
        GGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATG
        1738

        DD
        54007
        GGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATG
        53961

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes"
/db_xref="taxon:9598"
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DOE Joint Genome Institute.
Direct Submission
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287; Conservative
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Unpublished
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ACUY/331 200409 bp DNA linear HTG 22-JUN-2002
Pan troglodytes clone RP43-53A2, WORKING DRAFT SEQUENCE, 14
unordered pieces.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 200409)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
                                                       Submitted (04-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell Dive, Walnut Creek, CA 94598, USA On Aug 4, 2000 this sequence version replaced 9i:9256118.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88059 CACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCCTGTGGGGCCAGC 88118
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3 (bases 1 to 180596) DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 180596;
                                                                                                                                        www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                        www-shqc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
SHGC-32944 G29390
WI-6927 G06314
WI-19681 G21928
WI-9564 G06056.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 285; DB 9;
Pred. No. 6.7e-155;
0; Mismatches 2;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-296110"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.2%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.5 Matches 385; Conservative
                                           Direct Submission
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KEYWORDS
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Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankehurg, K., Bonnin, D., Bunck, J., Benton, J., Binage, K., Blankehurg, K., Bonnin, D., Bunck, J., Bente, S., Bireva, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C., Burch, P., Burkett, C., Burnell, K. L., Byrd, N. C., Carcon, T., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Cox, C., Coyle, M. D., Dederich, D. A., Delancy, K. R., Delancy, K. R., Delancy, K. R., Delancy, C. D., Denn, A. L., Ding, Y., Dinh, H. H., Douthmatter, K. J., Draper, H., Dugan-Rochs, S., Durbin, K. J., Barnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Ferraquto, D., Flagg, M., Forld, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garner, T., Garza, N., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Harr, Haye, P., Hawes, A., Houlandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Modah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Liu, M., Louiseged, Li, J., Liz, Lichtarge, O., Lieu, C., Liu, J., Liun, R., Martinez, E., Martinez, E., Martinez, R., Sont, J., Beery, J., Peters, L., Pickens, R., Parims, E., Sont, G., Martin, R., Martin, R., Martin, R., Wartin, R., W
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Center clone name: RA43-53A2
Center clone name: R443-53A2
Center clone name: R443-53A2
Center clone name: R443-53A2
Centering vector: Plasmid; M77789
Chemistry: Dye-terminator Bly Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 18781b bases at least Q40
Consensus quality: 193098 bases at least Q30
Consensus quality: 193098 bases at least Q30
Consensus quality: 193098 bases at least Q20
Consensus in Q2021 bases; agarose-fp estimation
Quality coverage: 0.3x in Q20 bases; sum-of-contigs estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 21, 2002 this sequence version replaced g1:21450389.
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Center code: BCM
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Worley, K.C.
Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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39511: gap of unknown length
61929: contig of 22418 bp in length
62029: gap of unknown length
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196238: gap of unknown length
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200409: contig of 2028 bp in length.
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Pred. No. 4.9e-102;
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Best Local Similarity 99.65
Matches 245; Conservative
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PRESENCE WITCHIGHTON Pan troglodyes clone RP43-33B16, WORRING DRARY SEQUENCE, B UNDOTEST A CTITIONS AND THE CONTROL OF THE CON
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                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
   Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 9.4x in Q20 bases; sum-of-contigs estimation
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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contig of 13171 bp in length
gap of unknown length
contig of 15040 bp in length
gap of unknown length
contig of 2410 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        f unknown length
g of 34346 bp in length
f unknown length
g of 20281 bp in length
f unknown length
g of 27892 bp in length
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49092: gap of unknown length
90442: contig of 41350 bp in length
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Pred. No. 4.9e-102;
O; Mismatches 1;
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/db_xref="taxon:9598"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO Sapiens.
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Matches 245; Conservative
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AC009125/c
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Summary Statistics
Consensus quality: 185671 bases at least Q40
Consensus quality: 183548 bases at least Q30
Consensus quality: 183548 bases at least Q30
Consensus quality: 189501 bases at least Q20
Estimated insert size: 189500; agarcse-fp estimation
Quality coverage: 3.4 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.23 in Q20 bases; sum-of-contigs estimation
** NOTE: This is a "working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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gap of unknown length
contig of 1006 bp in length
gap of unknown length
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of 1129 bp in length
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unknown length
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                                            Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                        Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                          Center Project Name: 595469
Center clone name: RPCI-11_492H8
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of 2708 b
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of 1738
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boushay, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McHeeters, R., Meldrim, J., Meneus, L., Norrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACO21951 79023 bp DNA linear HTG 13-JUL-2000
Homo sapiens clone RP11-396D24, LOW-PASS SEQUENCE SAMPLING.
ACO21951
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 79023)
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415 · 136514: gap of unknown length 515 150305: contig of 13791 bp in length 406 150405: gap of unknown length 406 163992: contig of 13587 bp in length 993 164092: gap of unknown length 996 187075: gap of unknown length 187075: gap of unknown length 187075: contig of 17969 bp in length 100 205044: contig of 17969 bp in length.
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54631 a 45103 c 45331 g 53992 t 5987 others
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Unpublished
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Pred. No. 4.2e-99;
0; Mismatches 1;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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TITLE JOURNAL COMMENT

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3580: contig of 892 bp in length

135980: gap of 100 bp

36880: contig of 892 bp in length

36880: contig of 900 bp in length

37974: contig of 894 bp in length

37974: contig of 898 bp in length

38962: contig of 888 bp in length

38962: gap of 100 bp

38974: contig of 912 bp in length

39974: gap of 100 bp

40899: contig of 912 bp in length

99974: gap of 100 bp

40899: contig of 925 bp in length

40899: contig of 925 bp in length
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31886: contig of 885 bp in length
32866: contig of 885 bp in length
2966: gap of 100 bp
33869: contig of 903 bp in length
3699: gap of 100 bp
34888: contig of 919 bp in length
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19: gap of 100 bp
23928: contig of 909 bp
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35880: cont
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Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Limmer, A. and Zody, M. Direct Submission
                                                                                                                                                     Submitted (22-3AN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6730807. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center Center for Genome Research Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
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897 bp in length
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f 886 bp in length
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f 919 bp in length
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f 919 bp in length
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f 912 bp in length
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f 894 bp in length
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f 913 bp in length
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contig of 884 bp in length
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5966:
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7964: con
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9945: con
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4972:
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2941:
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3960:
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1922:
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Description: 1st strand CDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTT]; double-stranded CDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the PCAIII sites can be used to isolate the CDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., Institute of Medical Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQIAQARAALCGTPPSLASAPWH
TLQVGWNVOLLPAGSASFVEVVSLWFREGORYSHAAGECARRATCTHTTQLWAATSSQ
LGCGRHLCSADQAAIEAFVCAYSPGGNWEVNGRTYTVPYKKGAMCSLCTASVSGCFRAW
DHAGGLCGECKRAQSGDPGVCYAASYWAVPEAFLSTOGGSCPACWETLFSESPPPL
TRGPQEPLSHELPEPRTSQHQHLPLPLSTWLHWQVLPSAVQPAVCARPVSGGCVLVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLHSETSPGRGHLLAVLLAFLGTTWAEVWPPQLQEQAPMARALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 22-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. I (bases I to 200409)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Briteat, M., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 TCCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCTGCGGGCTGACATGCGGGAGGCTG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes clone RP43-53A2, WORKING DRAFT SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 GACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 GACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="cerebellum cortex"
/clone_lib="macaque brain cDNA library QccE"
/dev_stage="adult"
64. .1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 115; DB.9; Length 2>v: Pred, No. 4.5e-55;
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
         PME18S-FL3 (Acc.No. AB009864)
                                                                                                                                                                                                                                                                                                                                                                                            1. 2900
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QccE-21387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="BaB41141.1"
/db_xref="G1:13676427"
                                                                                                                                                                                                                                                                                                  Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAAGCTGCGG]; 3' end primer [CGACCTGCAGCTCGAGCACA]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
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                            Draili (CACCATGTG)
Draili (CACCATGTG)
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       Vector:
R. Site1:
R. Site2:
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                                                                                                                                                                                                                                                                               Tokyo).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6261 CGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGCTCT 6320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6201 GAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAAGAAGGTGCCTGGTGTT 6260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         676 GAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTT 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   736 CGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGGCTCT 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB060195
AB060195.1 GI:13676426
Oligo capping; fis (full insert sequence).
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA, clone_lib:macaque brain cDNA library QccE clone:QccE-21387.
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB060195 2900 bp mRNA linear PRI 13-UT
Macaca fascicularis brain cDNA clone:QccE-21387, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 79023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                58984: gap of 100 bp
59895: contig of 911 bp in length
59995: gap of 100 bp
60882: contig of 887 bp in length
                                                                                                                                                      06: gap of 100 bp 62901: contig of 895 bp in length
                                                                                                                                                                                            100 bp
891 bp in length
                                                                                                                                                                                                                                              63992: gap of 100 bp
64887: contig of 895 bp in length
64987: gap of 100 bp
                                                                                                                                                                                                                                                                                             87: gap of 100 bp 65885: contig of 898 bp in length 85: gap of 100 bp 66885: contig of 900 bp in length 85: gap of 100 bp 67867: contig of 882 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           777; gap of 100 bp 66971; contig of 894 bp in length 771; gap of 100 bp 70884; contig of 913 bp in length 884; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                967: gap of 100 bp 68877: contig of 910 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 123; DB 2; I Pred. No. 9.4e-60;
882 bp
                                                                                                             p of 100 bp contig of 924 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Preα. ....
                                                                                                                                                                                                                        63892: contig of 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6%; Score 123;
58884: contig of
                                                                                                                                                                                                                                                                                                                                                                                   185: gap of 1
67867: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                       con.
66885: 7
                                                                                                           60982: gap of
61906: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70885 70984: gap of
                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                      62006:
                                                                                                                                                                                                                                                                                                                                                                                     66985:
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                                                                                                                                                                                                                                                                                                                                        65985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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66986
67868
                                                                                                                                                                                                                                                                                           64888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                unknown length
of 25417 bp in length
                                                                                                                                                                                                             unknown length
of 26077 bp in length
                                                                                                                           unknown length
of 22418 bp in length
                                                                                                   39411: contig of 39411 bp in length
                                                                                                                                                                                                                                                                                                            unknown length
of 11552 bp in
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                                                                                                                                                                                                                                                                                                                                                         unknown length
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/orqanism="Pan troglodytes"
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                                                                                                                        gap of contig gap of contig
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87546: 9
113623:
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196238:
198281:
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191838:
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Best Local Similarity 99.4'
Matches 165; Conservative
                                                                              be preserved
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191739
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196239
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198382
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169658
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SOURCE
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delangey, R. W., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, E., Kuleshi, A., Landry, N., Leal, B., Lewis, L.C.,
Kratson, E., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lij, Liz, Lichtarge, O., Liau, C., Liu, W., Loulseged, H.,
Lozado, R.J., Lux, Lucier, A., Lucier, R., Luna, R., Martinez, E.,
Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, S.,
Mosey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mouron, G.,
Oraguuye, N., Noviedo, R., Parton, B., Peery, J., Perez, L.,
Rives, M., Rojas, A., Rojubokan, I., Rojfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sutton, A., Svatek, A., Tabor, P., Tannerisa, M., Tannerisa, M., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Wang, S., Warley, W., Wulliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Warlington, D.,
Walliams, G., Wulliamson, A., Wleczyk, R., Wooden, S., Warlington, B., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Wallianson, A., Wleczyk, R., Wooden, S., Warlington
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 14 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-00T-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 200409) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 21, 2002 this sequence version replaced gi:21450389.
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 200409)
Worley, K.C.
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JOURNAL JOURNAL REFERENCE AUTHORS TITLE

TITLE

JOURNAL

REFERENCE AUTHORS

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COMMENT

TITLE

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AC009125 205044 bp DNA linear HTG 21-JUN-2000 HOMO Sapiens chromosome 16 clone RP11-492H8, WORKING DRAFT SEQUENCE, 60 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 128221 AGGTTAAGACCACATGCCTCATGTCCAAAGAGTCTCAGACCTTGCACAATGCCAGAAGT 128162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OY 1573 AGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAGT 1632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 115; DB 2; Length 200409; 99.4%; Pred. No. 4.8e-55; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 128101 GGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATG 128056
                                                                                                                                          gap of unknown length contig of 12707 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 11898 bp in length gap of unknown length contig of 2153 bp in length gap of unknown length contig of 2043 bp in length contig of 2043 bp in length
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55207 a 46732 c 45615 g 51554 t 1301 others
                                                                                                                                                                                                                      of 10083 bp in length
unknown length
of 11898 bp in length
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unknown length
of 17025 bp in length
                                                                         length
                                                                                                                     of 14250 bp in length
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DOE Joint Genome Institute
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Consensus quality: 188548 bases at least Q30
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Consensus quality: 188661 bases at least Q30
Consensus quality: 188661 bases at least Q30
Estimated insert size: 199500; agarose-fp estimation
Quality coverage: 3.4 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.23 in Q20 bases; sum-of-contigs estimation
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1159: gap of unknown 16
2165: contig of 1006 bg
2265: gap of unknown 18
3328: contig of 1063 bg
3428: gap of unknown 16
4435: contig of 1007 bg
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of 1613 }
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Center clone name: RPCI-11_492H8
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AK096051
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Homo sapiens kidney cDNA to mRNA, clone_lib:KIDNE2
                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                  /clone_lib="RPCI human BAC library 11"
54631 a 45103 c 45331 g 53992 t 5987 others
186975: contig of 22883 bp in length
187075: gap of unknown length
205044: contig of 17969 bp in length.
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/clone="KIDNE2010750"
/tissue_type="%idney"
/clone_lib="KIDNE2"
/note="Loning vector: pME18SFL3"
180. .641
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                                                                                                                                                                                                                                         Query Match 5.8%; Score 109; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 109; Conservative 0; Mismatches
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NEDO human cDNA sequencing project
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                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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                                                         Location/Qualifiers
1. .205044
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Isogai, T. and Yamamoto, J.
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AC021951. GI:9154380
/protein_id="BAC04687.1"
/brotein_id="B1:21755445"
/db_xref="G1:21755445"
/translation="MLDWGGRRRKEDOGWGOGGTPRSAVAGAWRNPWFGGAPDRGLRE
/translation="MLDWGGRRRKEDOGWGOGGTPRSAVAGAWRNPWFGGAPDRGLRE
PGLAPPPSPHRGSLPPPOPOCHSAHACCTWSLSQPRSIAMPHVPCTHHTPLPSCFPRAG
THAYSAVCWVQVPPSSGCLTFSPHPSPEQEGEFLAPLPAQPPAQLGPAPGG"
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Birren B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
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* sequencing reads that have not been assembled into
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------- Project Information
Center project name: L5885
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100.0%; Pred. No. 2.5e-43;
tive 0; Mismatches 0;
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contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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of 901 bp in length
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of 897 bp in length
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of 894 bp in length
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                                                                                                                                                                                                                                                                                                                                                                  100 bp
of 913 bp in length
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f 919 bp in length
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f 912 bp in length
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f 919 bp in length
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879 bp in length
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contig of 897 bp
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29902: contig of 873 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   967: contig of gap of
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31981: gap of 1
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30896; contig
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14924: cr
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12953: con
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15910: con
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9945: con
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1010 1922: co
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3960: co
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5966: cc
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in length in ŗ in in 73 32956; gap of 100 bp 100 3989; gap of 100 bp 100 34888; contig of 910 bp 100 34888; contig of 910 bp 100 34888; contig of 910 bp 100 35880; contig of 910 bp 100 35880; contig of 910 bp 100 37874; contig of 912 bp 100 37874; contig of 912 bp 100 37874; gap of 100 bp 175 39874; contig of 912 bp 100 37874; contig of 912 bp 100 37874; contig of 912 bp 100 37874; gap of 100 bp 100 bp 100 57878 bp 10 6 64987: gap of 100 bp 65885: contig of 898 bp ir 65885: gap of 100 bp 66885: gap of 100 bp 1 33870 33969: 36881 14035

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Query Match
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E. Prescott,A. and Roe,B.A.

Mus musculus BAC Clone rp23-340n2

L. Onpublished

E. Chases 1 to 200755)

S. Prescott,A. and Roe,B.A.

Direct Submission

E. John College 1 to 200755)

S. Direct Submission

E. John College 2 to 200755

S. Direct Submission

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E. John College 2 to 200755

E. Direct Submission

E. Submitted (20-Aug-2002) Department Of Chemistry And Biochemistry, on Aug 20, 2002 this sequence version replaced gi:22213237.

Center: Department Of Chemistry And Biochemistry

The University Of Oklahoma

Center code: UOKNOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zυυ/၁၁ bp DNA linear HTG 20-AUG-2002 Mus musculus chromosome 8 clone rp23-340n2 strain C57BL/6J, WORKING AC093451
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                                                                                                                                                                                                                                                                   53193 TGTGGGGCACCTGCAAGTGGGGTGGAACATGCAGCTGCTGCCGCGGGGCTTGGCGTCCT 53134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 33810: contig of 33810 bp in length
* 33811 70420: contig of 36510 bp in length
* 70421 70520: gap of unknown length
* 70521 132973: contig of 62453 bp in length
* 132974 133073: gap of unknown length
* 132974 133073: gap of unknown length
* 132974 133073: gap of unknown length
* 132974 130075: contig of 67682 bp in length.

Location/Qualifiers
e
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                                                                                                                                                                                               ;
                                                                                                                                         Length 79023;
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68878 68977: gap of 100 bp
68978 68871: contig of 894 bp in length
69872 69971: gap of 100 bp
70885 70984: gap of 100 bp
100 bp
                                                                                                                                                Score 79; DB 2; I
Pred. No. 6.6e-34;
                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                    100.0%;
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                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 79; Conservative
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RAUGADAM, Adams.C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Aliben, C., Burch, P., Benton, J., Benton, C., Burch, P., Burkett, C., Burch, R.L., Byrd, N.C., Carron, T., Burach, C., Chen, G., Chen, G., Chen, G., Chen, R., Chen, G., Chen, G., Chen, R., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Delandy, R.R., Delader, D., Dathorne, S.R., David, R., Delandy, R.R., Delader, D., Dathorne, S.R., David, R., Jouthart, C., Edgar, D., Edwards, C.C., Elbid, C., Escotto, M., Farnhart, C., Edgar, D., Flang, N., Frockl, J., Poster, P., Frantz, P., Ganls, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gall, R., Harris, C., Harris, K., Harr, M., Havlak, P., Hawes, A., Hennandez, O., Hodgson, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Lucier, A., Garner, T., Joule, J., Good, J., Kovar, C., Lida, S., Huber, J., Jacobson, B., Jia, Y., Lucier, A., Lucier, R., Lucier, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus clone CH230-122N13, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                               Length 200755;
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                                                                                                                                                                                                                                           2.3%; Score 44; DB 2; Lv 100.0%; Pred. No. 2.4e-13; tive 0; Mismatches 0;
/db_xref="taxon:10090"
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Rattus norvegicus
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Worley, K.C.

Direct Submission
AL Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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6 Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA
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NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced g1:17967675.
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                         Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: project Information
Center project name: GGFR
Center clone name: CH230-122N13
Center clone name: CH230-122N13
Sequencing vector: plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 131950 bases at least Q40
Consensus quality: 140067 bases at least Q20
Consensus quality: 146790 bases at least Q20
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GGAKMABGGVQSPPDIAQLSILGILESLKAYPRAMARLKDTVALAAREKPDVAVLIDS

WGFNIRLAHALRRLDPTLFDVKYVAPQVWAYREGRAGALAKAVDLLLSIQPMDKAYFD

AAGLONFFVGRALAKRFDHADPGRLRAAIGAAASQOILLVLFGSRPSFIERVWRAFE

ACGLONFFVGRPDLHIVVPAXTVABAVKARVAGWPFRAHYIEDEGLKDDAFLAGDVAL

ACGGGTVTTELALAGRPWVVGYKTGAVTYAIVKRLMKPRHITLFNIAAGKAVAPELIQH

ACEGGGLAREVALRLDDPDLKQRQTAEQYAALDRMGRGMPDPSEAAABALLDFLSARG
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Caulobacter crescentus CB15 section 191 of 359 of the complete
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/protein_id="AAK23884.1"
/db_xref="G1:13423362"
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SOURCE
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GANSCVDRGAFGDTTIGENTKIDNLVHVAHNVRIGRNCVLAAYTGVSGSTVVGDGVAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MPDPRFFDSLGPALLSELAQAGAATLADAALGERVITHAAPLDA
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GRYSFIGGLAAVTKDV1PYGSVWGNHAHLEGLNLVGLKRRGFPRETINALRAAYRLMF
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dehydratase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="conserved hypothetical protein"
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complement(2907. .3386)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3389. .4408)
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                                                                                                                                                                                                                                                                                                                                                                   complement(2119. .2910)
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LOCUS
                                                                        RESULT 25
HS366N23/c
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LDGNLLAQILPVRTGQLYEDERIEQATDALTFAAGAAGFAFVDVRPRYVPNRETKTVD
VFGVRGGFRYVORIDIVGNFRTLDYVLRRELEVAEGDAY WRTVLVDRSKNNMRRLGF
FKEVEIEDAPGSARPTSLRVVVEDQPTGELSFSAGSISIDKLVLDVGITERNFRGRG
ONLRARASVGSLRQIDFGFSEPRFLGRNLVAGVNLYTFRXDLSFFAAYDTKSVGGDV
RFGFPLTNDSSMSLRYTVRQDEVSVADSLCASGSVSQILCLQRGAYITSLIGYGLRID
ALEQQAATLQAKANAWQRKGQLRQKEVEATEQKALSRVYQELNTPIQQVYQAQKCSVL
LDREAVMLANPAMDITDAVVAALDARIKTLTFDRERLDQQVPGAAALQPTNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                 YLPIQPGDFWDSQRLDLALKTLARTDLFADWY IEMIGGDLWVKVVENPIINQVYFEGN
SSLKEDKLKDEVQIRPRGIFTRAKVQADVQRIIELYRRSGRISATYPRKVVELPQKRV
DLVFEINEGAKSGVLGINFLGNAEYSDNDLRDVIVTKESRWYKILTSNDNYDDDRIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWGGDNVRINDRFYRGGTSFRGFEIAGIGPRDISSSFNSMGAKLYAISTFELTVPTFL
PRQYGIKAALFSDVGTAGLLDDVDRQRSPGVFDPNIKDNLGLRASAGISIDWKSPMGP
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VERLIEGARRWKPSLAVIEDESRLDDLRAGLAGTGVEAAAGADAVRDAAAMGADWVMS
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FAWPDRLPWPAPRLDLAAYGQLTFESPDVERFPAIGIAREALRLGGGAPAANNAANEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRNDPINPTRGWFADLNQDLAGVGGDVKYLKTEADAGWYWGFTKDLVFSATGSFGYIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGFKPGDVILKADNROIRSPODIOGYVALRANMPIDFAVERDGRTVHLTATPRLVER
ONEISGRVKVGELGLRSAPGGRFERSSLLSAIPDATVEVWDMIKTIARYLGRLMGOL
PADOISGIIGIGHTAGAVTNGVVEQAPNGKALAIGLIYSQFWLIASLSVSIGFMNLLP
IPVLDGGHLVWYAYEAVAKRPLRAEFQAAGFRAGLALLIGFMLFAAWNDLNRYDVFKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="identified by match to TIGR protein family HMM TIGR00054"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="membrane-associated zinc metalloprotease, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="identified by match to TIGR
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complement(7484. .8680)
/gene="CC1916"
                                                           complement(5103. .7412)
                                                                                                                         complement(5103. .7412)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(8703. .9902)
                                                                                                                                                                                                                                                                             /transl_table=11
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Best Local Similarity 100.0
Matches 23; Conservative
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Submitted (24-JUL-1998) E-mail enquiries: humquery@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
Clone requests: clonered repeated from overlapping clones.
Where differences are found these are annotated as variations
Where differences are found these are annotated as variations
Together with a note of the overlapping clone name. Note that the
Variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
This sequence is the entire insert of clone 366N23. This sequence
has been finished according to sequence map criteria as follows. An
according to resolve all sequencing problems, such as
HS366N23 98517 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from clone 366N23 on chromosome 6q27. Contains two genes similar to consecutive parts of the C. elegans UNC-93 (protein 1, C46F11.1) gene, a KIAA0173 and Tubulin-Tyrosine Ligase LIKE gene, a Mitchic Readback Control Protein MADP2 Homolog LIKE pseudogene and the last two coding exons of the TCP10 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 366N23 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacper.med.buffalo.edu/ VECTOR: pcrApC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Alusx repeat: matches 298. .132 of consensus" complement(6290. .6460) /note="match: GSS B89104"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9060. 9261
/note="MLTIC repeat: matches 201. .412 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1 repeat: matches 3033. .5390 of consensus"
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/note="AluJb repeat: matches 1. .123 of consensus"
complement(7954. .8263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1895. .9052 'note="MLT1B repeat: matches 2. .171 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .889 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 30. .238 of consensus"
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                                                                                                                                                                                                                                                             AL021331.1 GI:3355532
HTG: C46F11.1; KIAA0173; MADP2; Mitotic Feedback Control;
T-complex; TCP10; Tubulin-Tyrosine Ligase; UNC-93.
Homo sapiens.
Homo sapiens
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/note="L1PA2_repeat; matches 3.
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/note="MLT1C repeat: matches 2.
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/db_xref="taxon:9606"
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/clone_lib="RPCI-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 98517)
Phillips, S.
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/note="MIR r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .98517
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Gaps

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DB 1; Length 12977; 0.5; 0; Indels

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HSS171M_1
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/gene="dJ366N23.1"
/product="dJ366N23.1"
/product="dJ366N23.1" (putative C. elegans UNC-93 (protein
1, C46F11.1) LIKE protein)"
/note="match: ESTS W78931 T60341 T60316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
join(29839. .29925,32866. .33047,34381. .34610,36294. .36454)
/gene="dJ366N23.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement(14212. 14821)

Complement(14848 .14943)

Complement(14848 .14943)

Complement(14848 .14943)

Anote="Information and the property of consensus"

Anote="17 copies 6 mer gagaga 81% conserved"

17590. 17627

Anote="19 copies 2 mer ag 82% conserved"

18118. 18546

Anote="match: GSS AQ022355"

Anote: Match: GSS AQ022355"

Anote:
9385. .9530
/note="MERSA repeat: matches 5. .177 of consensus"
9616. .9688
/note="MESA repeat: matches 106. .177 of consensus"
9963. .10228
                                                                                                                                                                                                                                                                                       /note="MER34 repeat: matches 344. .520 of consensus"
10705. .10768
                                                                                                                                                                                                                                                                                                                     /note="MER45 repeat: matches 58. .119 of consensus" complement(10798. .11387)
/note="MER4B repeat: matches 575. .1 of consensus" complement(11907. .12307)
/note="MER4B repeat: matches 573. .188 of consensus" 12989. .13077
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// note="MIR repeat: matches 156, .2 of consensus" complement(28919, .29074)
// note="MIR repeat: matches 204, .50 of consensus"
                                                                                                                                                                                                               /note="MER34 repeat: matches 3. .246 of consensus"
10356. .10535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="3 copies 31 mer 87% conserved"
25813. .25941
/note="MIR2 repeat: matches 1. .128 of consensus"
26032. .26107
26034. .26117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 50. .140 of consensus" complement(14212. .14821)
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/note="12 copies 6 mer gtgtgt 85% conserved"
26034. .26099
/note="3 copies 22 mer 83% conserved"
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/note="19 copies 2 mer ac 100% conserved"
26799. .26834
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/note="3 copies 22 mer 82% conserved"

25046. .25346

/note="AllSx repeat: matches 2. .302 of 02444. .25536
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/note="3_copies 28 mer 81% conserved"
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join(<42283...43482,44264...44399,46128...46259,53536...54363)
/gene="dJ366N23.2"
/product="dJ366N23.2 (putative C. elegans UNC-93 (protein 1, C46FI1.1) C-terminal LIKE protein)"
/note="match: ESTS W92071 H77443 W85699 R16618 AA702150
W92075 H47279 R16560 H57967"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .53801)
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RAVLYVLGAYTHVSCMIALLLWRPRADHLAVFFVFSGLWGVADAVWQTQNNALYGVLF
EKSKEAAFANYRLWEALGFVIAFGYSMFLCVHVKLYILLGVLSLTMVAYGLVECVESK
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                                                                                                                                                                                           /translation="MDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEBGLGVTALS
TLYGGMLLSSWFLPPLLIERLGCKGTTILSMCGVAFSVGRFSWYFLTFYSTLLFTSTLLGL
GAAPLWSAQCTYLTTGGNTHAREAGKRGKDWVNQYFGTFFLIFFLSSGWWGNLISSLVF
GQTPSQGFTLPFBQQLTATGGNTHAREAGKRGKDWYNQYFGTFFLIFCTSSTGPGQG
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/product="dJ366N23.2 (putative C. elegans UNC-93 (protein I. d6FIL.1) C-terminal LIKE protein)"
/protein_id="CAAJ6150.1"
/db_xref="GT:335534"
/db_xref="GT:335534"
/evidence=not_experimental
/product="dJ366N23.1 (putative C. elegans UNC-93 (protein
/p. c46F11.1) LIKE protein)"
/protein_id="CAA16149.1"
/db_xref="GI:3355533".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: proteins 023024 093380; true start codon could be located on a yet undisclosed upstream exon; the matches of this gene with the C. elegans are contiguous with the matches of dJ366N23.1 (with a gap), but it appears that what is one gene in worm are at least two separate genes in human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence-not_experimental
join(42291. .42482,44264. .44399,46128. .46259,53536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER44C repeat: matches 728. .476 of consensus" complement(41382. .41456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Alusx repeat: matches 1. .295 of consensus" 37491. .37574 / .70te="3 copies 28 mer 81% conserved" complement(41121. .41379)
                                                                                                                                                                                                                                                                                                                                                    31232. .31299
//note="2 copies 34 mer 97% conserved"
//note="3.2412
//note="MIR2 repeat: matches 68. .146 of consensus"
complement(36704. .36786)
//note="MER3 repeat: matches 137. .52 of consensus"
//note="MER3 repeat: matches 137. .52 of consensus"
//note="MER3 repeat: matches 137. .52 of consensus"
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100.0%; Pred. No. 2;
tive 0; Mismatches 0; Indels (
                                                                                                                                                            /db_xref="SPTREMBL:075651"
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/gene="dJ366N23.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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Fragment Name Begin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Worley,K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                           Submitted (27-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases I to 134151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG 18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 91% of reads
Chemistry: Dye-primer Bodipy: 91% of reads
Chemistry: Dye-primer Big Dye: 9% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 122214 bases at least Q40
Consensus quality: 132434 bases at least Q20
Consensus quality: 133922 bases at least Q20
Estimated insert size: 134530; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3823: contig of 3823 bp in length 8764: contig of 4841 bp in length 8864: gap of unknown length 8864: gap of unknown length 20193: contig of 11329 bp in length 41239: contig of 20946 bp in length 41339: gap of unknown length 59870: gap of unknown length 59870: contig of 18531 bp in length 59970: contig of 18531 bp in length 89814: contig of 28844 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 others
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                                                                                                                                                                                                                                                                                                                                           Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                             ---- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: HCCN
Center clone name: RP11-62D5
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8765
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59871
59971
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88915
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20294
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                              JOURNAL
                                                                                                                                 AUTHORS
                                                                                                        REFERENCE
                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
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AC125935
                                                                                                                                                                                                                                                             COMMENT
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HSSI7IM_0
HSSI7IM_1
HSSI7IM_2
HSSI7IM_3
Continuation (2 of 4) of HSSI7IM from base 100001 (AJ239326 Homo sapiens chromosome 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RS MURRAY, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabardoks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benchon, J., Binager, K., Blankehurg, K., Bonnin, D., Burbell, K.L., Brown, M., Bryant, N.P., Burbell, K.L., Byrd, M. C., Carron, T., Elarage, K., Elarkehurg, K., Bonnin, D., Burbell, K.L., Byrd, N.C., Carron, T. E., Chen, Z., Chowdhry, I., Christopoulos, C., Carron, T. C., Coyle, M.D., Dathonne, S.R., David, R., Delane, K.R., Deladado, O., Doar, Carroll, L., Dederich, D. A., Delane, K.R., Dragaro, D., Edyado, O., Denn, A.L., Ding, Y. Dinh, H.H., Douthwaite, K.J., Dragar, H., Dugan-Rocha, S., Durbin, K.J., Palls, T., Ferraguto, D., Edyards, C.C., Elhaj, C., Escotto, M., Call, R., Correll, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harris, K., Harris, P., Hales, S., Hamilton, K., Harris, C., Harris, K., Houser, W., Gunaratne, P., Hales, S., Hamilton, K., Harris, K., Houser, W., Gunaratne, P., Hales, S., Hamilton, K., Harris, K., Harris, K., Han, W., Holloway, C., Hollins, B., Jacobson, B., Jis, Y., Johnson, R., Jolivet, S., Joudh, S., Marlincz, E., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, U., Kovar, C., Li, J., Liu, W., Luux, Lux, X., Ludy, M., Martin, R., Martinez, E., Mahris, P., Martin, R., Martin, M., Massey, E., Mawhiney, E., Martin, R., Martin, R., Martin, M., Massey, E., Mawhiney, E., Martin, R., Wohand, Y., Luux, K., Luux, K., Luux, K., Luux, K., Luux, K., Luux, K., Moser, M., Neal, D., Newison, R., Morter, S., Soott, G., Shen, H., Shotter, S., Chun, M., Toward, S., Soott, G., Shen, H., Shotter, S., Stort, G., Shen, H., Shotter, S., Soott, G., Shen, H., Shotter, S., Thous, S., Ward, Wooden, S., Ward, Woore, S., Ward, Wooden, S., Ward, Woore, S., Ward, Wooden, S., Ward, Woore, S., Ward, Woore, S., Ward, Wooden, S., Ward, Woore, S., W
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 12 clone RP11-62D5, WORKING DRAFT SEQUENCE, A propordered pieces.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                          ;
0
                                                                                                                                                          DB 2; Length 110000;
2;
                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                     Score 22;
                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                         Db 30521 GGGCIGIGGGCGCACCTGTGC 30542
                                                                                                                                                                                                                                                             605 GGGCTGTGGGCGGCACCTGTGC 626
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                                                                                                                                                                1.2%;
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1 (bases 1 to 134151)
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Worley, K.C.
                                                                                                                                                                                                                 Conservative
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                                                                                                                                                          Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC079318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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AC079318
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KEYWORDS
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AUTHORS
TITLE
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JOURNAL
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SOURCE

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Ratus, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabess 1 to 165645)

Munny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabers, C., Are, J.R., Ayele, M., Bendin, D., Barbarta, J., Bowles, S., Britava, M., Brown, E., Brown, M., Bryant, N.C., Burch, P., Burch, P., Burkett, C., Burrell, R.L., Byri, N.C., Carron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdiry, I., Christopoulos, C., Chen, R., Correll, D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Barnhatt, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, R., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunratto, P., Hales, S., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernadez, O., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernadez, C., Harris, K., Hauber, J., Hulyk, S., Hume, J., Jackson, E., Lidgen, A., Garner, T., Garza, N., Gollins, B., Jacobson, B., Jia, Z., Johnson, R., Jolivet, S., Jouch, S., Loucker, M., Mapla, M., Marlin, R., Marlin, R., Martin, R., Martin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus norvegicus clone CH230-225E7, *** SEQUENCING IN PROGRESS ***, 67 unordered pieces.
AC125935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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Center clone name: CH230-225E7
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Worley, K.C.
Direct Submission
                                                                                                             AC125935.1 GI:21671541
HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                    Rattus norvegicus
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will
                  Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 103958 bases at least Q30 Consensus quality: 113163 bases at least Q30 Consensus quality: 118563 bases at least Q20
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    (bases 1 to 178413)

                                               Plumb.B.
Direct Submission
Direct Submission
Submitted (28-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 26, 2002 this sequence version replaced gi:21614845.
                                                                                                                                                                                                                                          Assembly program: XGA44; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 175430 bases at least Q40
Consensus quality: 17648 bases at least Q30
Consensus quality: 176809 bases at least Q30
Insert size: 177413; sum-of-contigs
Insert size: 190090; 0.7% error; agarose-fp
Quality coverage: 6.21x in Q20 bases; sum-of-contigs Quality
coverage: 5.87x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently a consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
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/note="assembly_fragment:00378
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/db_xref="taxon:10090"
/chromosome="4"
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Nuzny, D.W., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Banton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burkett, C., Burnell, K.L., Bryd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, C., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dednery, K.R., Dalgado, O., Davy-Carroll, L., Dederloth, D.A., Delaney, K.R., Dalgado, O., Davy-Carroll, L., Dederloth, D.A., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Ellag, N., Ford, J., Foster, P., Garza, N., Falls, T., Ferraguto, D., Guevara, W., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Garcia, A., Garner, T., Garza, N., Gill, R., Garrell, J.H., Garral, J.H., Hamilton, K., Han, J., Hernandez, O., Harris, C., Howard, S., Huber, J., Hamilton, K., Han, J., Hernandez, J., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, J., Howard, S., Huber, J., Jak, K., Jahnson, R., Jacobson, B., Jia, Y., Johnson, R., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Lealy, N., Leal, B., Lee, E., Lewis, L.C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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fragment_chain:1"
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/note="assembly_fragment:01991
fragment_chain:1"
104938..178413
fragment_chain:1"
25881. .48226
7.note="assembly_fragment:00581
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48327. .65871
/note="assembly_fragment:01212
fragment_chain:1"
65972. .74331
/note="assembly_fragment:02027
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Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R.,
Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P.,
Mador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner G.,
Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M.,
Moyren, A., Mayuen, N., Nelson, D., Newtson, J., Newtson, N.,
Nayven, A., Mayuen, N., Nayven, N., Nickerson, E., Nwokenkwo, S.,
Oguh, M., Okwuonu, G., Oragunye, N., Oriedo, R., Pace, A., Patron, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
Ogul, M., Cayer, Y., Rives, M., Rojas, A., Rojubokan, I., Sparks, A.,
Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A.,
Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tang, H.,
Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D.,
Vinson, R., Wall, R., Wang, S., Ward Moore, S., Warren, R.,
Washington, C., Watlington, S., Williams, G., Williamson, A.,
Direct Submission
Inver, Submission
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Worley K.C.

Worley K.C.

Worley A.C.

Worley Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Worley K.C.

Worley K.C.
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INFORMATION: http://www.ngsc.bcm.tmc.edu/ or email
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Submitted (05-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Pavior Plaza, Houston, TX 77030, USA
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Submitted (01-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 189456)
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5 (bases 1 to 189456)
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STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

ANNOTATION OF FEATURES:

us-09-944-896-49.olil0.rge

Repeats are identified using RepeatMasker (A. Smit and P. Green,

unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

OUALSTAT-REPORT------

197276 1.32507e-05 0.00304649 22 0 197844 ----- Summary Statistics -----Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus: values in estimate: Contig length: Phrap

gtatgtaatt(t)actgggaaga
aataccttta(a)tgtcagtacc tacctttaat(g)tcagtaccaa cctttaatgt(c)agtaccaaca ctttaatgtc(a)gtaccaacaa gctgggatta(g)aaaaacatat aataaaactg(t)tgctcatcaa tacatatg(t)atatatacat tatacatatg(t)acatatatac tttaatgtca(g)taccaacaaa tatgttaatg(g)atgataagat atatatacgt(a)tatatgtata tatatatacg(t)atatatgcat cggatatatg(c)gatatataca cggatatatg(c)gatatataca cggatatatg(c)gatatataca tatggacaac(t)tcttcgcccc atggacaact(t)cttcgcccc tggacaactt(c)ttcgccccg ggacaacttc(t)tcgcccccgt gcgacaaggt(g)ctgatgccgc cgacaaggtg(c)tgatgccgct Edited+Context Consensus changing edits cctttantnt(n)nntaccaaca ctttantntn(n)ntaccaacaa tatgttaatg(n)atgataagat gctgggatta(n)aaaaacatat gtatgtaatt(n)actgggaaga aataccttta(n)tntnnntacc tacctttant(n)tnnntaccaa tttantntnn(n)taccaacaaa aataaaactg(n)tgctcatcaa atatatacgt(g)tatatgtata cggatatatg(n)gatatataca tacatatatg(g)atatatacat tatatatacg(n)atatatgcat cggatatatg(n)gatatataca cggatatatg(n)gatatataca tatacatatg(g)acatatatac tatggacaac(n)nnntcgcccc atggacaacn(n)nntcgcccc tggacaacnn(n)ntcgccccg gcgacaaggt(n)ntgatgccgc cgacaaggtn(n)tgatgccgct ggacaacnnn(n)tcgccccgt Original+Context Position 44170 159989 197647 197648 197649 197650 197700 160107 160184 160222 160282 160409 160423 460 462 463 464 23959

Distribution of Quality < 40 Bases ---5001 4501 33001 32001 1501 501 bases

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality sequenced by alternate of compressions and repeats; all regions were covered by at least as sembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-36P22 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pBACe3.6.

	* * * * * * * * * * * * * * * * * * * *
	5 10 15 20 25 30 35 40 Phrap Value Range
FEATURES Source repeat misc_f	Version: 1.01 Version: 1.01 1 Vorg Ab. Chr Clor Cl
Query Match Best Local Matches 2 Qy 1779 CTC Db 104060 CTC	egion Similari Z; Constructaccaccru
RESULT 31 AL591488 LOCUS DEFINITION ACCESSION VERYORDS SOURCE OUTSIAN	AL591486 Mouse DNA linear ROD 05-APR-2002 Sequence. Sequence. AL591488 AL591488.7 GI:17065727 HTG.
REFERENCE AUTHORS TITLE JOURNAL	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Pearce, A. Direct Submission Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton.
COMMENT	אטכט מי

FEATURES

ORIGIN

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17555 175351: gap of 100 bp 175352 181328: contig of 5977 bp in length 181329 181428: gap of 100 bp 181428: gap of 2435 bp in length 181429 183644 189563: contig of 100 bp 183964 195169: contig of 11206 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 195269; gap of 100 bp 0
0 205272; contig of 10003 bp in length.
Location/Qualiflers
                                                                                                                                                                                                                                                     24967 125066; gap of 100 bp
125067 142955; contig of 17889 bp in length
                                                                                                                                                                                                                                                                                                     142956 143055: gap of 100 bp
140056 161736: contig of 18681 bp in length
161737 161836: gap of 100 bp
1618197 169189: contig of 7353 bp in length
169290 175251: contig of 5962 bp in length
                          80234: gap of 100 bp
83646: contig of 3412 bp in length
83746: gap of 100 bp
96061: contig of 12315 bp in length
                                                                                                                                                            103411: gap of 100 bp 122508: contig of 19097 bp in length
80134: contig of 30381 bp in length
                                                                                                         96062 96161: gap of 100 bp 96162 103311: contig of 7150 bp in length 103312 103411: gap of 100 bp
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fragment_chain:2"
fragment_chain:2"
fragment_that955
fragment_chain:3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL353591 205272 bp DNA linear HTG 13-JUN-2001
Homo sapiens chromosome 6 clone RP11-366H19, *** SEQUENCING IN
PROGRESS ***, 18 unordered pieces.
                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 205272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (12-JUN-2001) Sanger Conterposests: cloneerequests: cloneerequests: cloneerequests: clonerequests (Sanger Center
Genter: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; 1008552; 100% of reads Sequencing vector: plasmid; 1008552; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 197267 bases at least Q40 Consensus quality: 200442 bases at least Q20 Insert size: 203572; sum-of-contigs Insert size: 183107; 13.0% error; agarose-fp Quality coverage: 3.30% in Q20 bases; sum-of-contigs coverage: 3.75% in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                         DB 10; Length 191494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4260 4359; gap of 100 bp
4260 4359; gap of 100 bp
4360 26102: contig of 21743 bp in length
26103 26202; gap of 100 bp
26203 28547; contig of 2345 bp in length
28548 49653; cantig of 2100 bp
49654 49753; gap of 100 bp
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46072 c 46038 g 49696 t
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL353591
AL353591.5 GI:9930866
HTG: HTGS_PHASE1; HTGS_CANCELLED.
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100.0%; Pred. No.
                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 DD 38657 ATGAATCAGCTGAAAAAAAA 38678
                                                                                                                                                                                                                                                                                                                                         1852 ATGAATCAGCTGAAAAAAAAA 1873
                                                                                                            /chromosome="2"
                                      1. .191494
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 22; Conservative
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                                           source
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AL353591/c
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                                                                                                                                                                             BASE COUNT
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AUTHORS
TITLE
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KEYWORDS
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COMMENT

SOURCE

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8003 8102: gap of
8103 8749: cor
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State 1 to 208613)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Choepel, Y., EitzHugh, M., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,

Ferreira, P., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R.,

Jones, C., Kamat, A., Karatas, A., Marquis, N., Matthews, C.,

Macdonald, P., Major, J., Levine, R., Liu, G.,

Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

Mcarthy, M., McFwan, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, D., O'Neil, D.,

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Raymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R.,

Seaman, S., Severti, M., Travis, N., Trigilio, J., Vassillev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Direct Submission.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC093464 208613 bp DNA linear HTG 26-AUG-2001
Mus musculus clone RP23-225L1, WORKING DRAFT SEQUENCE, 23 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                      2; Length 205272;
                                                                                                                                                                                                                                                                                 vector_side:right"
53785 a 47341 c 47491 g 54940 t 1715 others
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 208613)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-22511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 95161 GGCCAGGGAGTGAGTGTTAGAA 95140
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                                                                                                                                                                                                                                                         clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
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  misc_feature
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AUTHORS
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JOURNAL
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Web site: http://www-seq.wi.mit.edu

Center code: WIBR

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consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                        Center close can memorize 222_L1

Sequencing vector: Plasmid; n.5 100% of reads
Sequencing vector: Plasmid; n.5 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 108685 bases at least Q40
Consensus quality: 202938 bases at least Q30
Consensus quality: 204617 bases at least Q30
Insert size: 200000; agarose-fp
Insert size: 206043; sum-of-contigs
Quality coverage: 9.3 in Q20 bases; sum-of-contigs
Quality coverage: 9.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 1711; gap of 100 bp 1100 bp 12 1711; gap of 100 bp 12 1718. gap of 100 bp 12 1719; gap of 100 bp 12 175; gap of 100 bp 12 175; gap of 100 bp 12 175; gap of 100 bp 100 bp 12 1776; gap of 100 bp 100 bp 1776; gap of 100 bp 1777; gap of 100 bp 1775; gap of 100 bp 1775; gap of 1775; g
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105251 176270: contig of 71020 bp in length
176271 176370: gap of 100 bp
176371 208613: contig of 32243 bp in length.
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63154: contig of 15454 bp in length
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10621: contig of 939 bp in length
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/db_xref="taxon:10090"
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9582: contig of
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Submitted (08-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA on Aug 8, 2002 this sequence version replaced gi:21426746.
                                                                                                                         2 (bases 1 to 223898)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 223898)
McPherson, J.D. and Waterston, R.H.
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 223898)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; 0%
Sequencing vector: plasmid: 100%
Sequencing vector: plasmid: 100%
Chemistry: Dye-terminator Big Oye : 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 221926 bases at least Q40
Consensus quality: 223804 bases at least Q20
Insert size: 224000; agarose-fp
Insert size: 230073; sum-of-contiss
Quality coverage: 13.05 in Q20 bases; sum-of-contiss
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1121: gap of unknown length
5763: contig of 4642 bp in length
5663: gap of unknown length
55886: contig of 50123 bp in length
52086: contig of 50123 bp in length
520814: contig of 166728 bp in length
222814: gap of unknown length
223359: contig of 445 bp in length
223459: gap of unknown length
223389: contig of 439 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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/note="assembly_name:Contig48"
56087. .222814
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/clone="RP23-81K14"
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Mus musculus
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Mus musculus chromosome UNK clone RP23-81K14, WORKING DRAFT SEQUENCE, 6 unordered pieces.
AC124604
AC124604.2 GI:22138688
HTGS, PHGSLPAST; HTGS_EULTOP.
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                /clone_lib="RPCI-23 Female Mouse BAC"
1. .8002
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53175 c 52217 g 50228 t
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13260. .13938
/note="assembly_fragment"
14039. .15029
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note="assembly_fragment"
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17112. .17861
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4852. .31676
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Z64522 bp DNA linear HTG 14-AUG-2002 DRAFT SEQUENCE, 13 unordered pieces.
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Jiang.X., Song,L. and Roe,B.A.
Mus musculus BAC Clone rp23-11f20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-AUG-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
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On Aug 14, 2002 this sequence version replaced gi:22165141
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                                                                                                                                                     DB 2; Length 223898;
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The University Of Oklahoma
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gap of unknown length
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                                                                                                                                                Query Match
1.2%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches
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Jiang, X., Song, L. and Roe, B.A.
Direct Submission
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3 (bases 1 to 264522)
Jiang, X., Song, L. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                          Db 157107 CCTGGCCCTCCTTGGCACCACC 157128
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                 misc_feature
                                                     misc_feature
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AC090437
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 34000).

S Hattori, M., Eujiyama, A., Taylor, T.D., Watanabe, H., Yada, T.,
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Hornischer, K., Brandt, P., Scharfe, M., Schoen, O., Desario, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library" 63608 c 62531 g 67771 t 1222 others
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Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing
Consortium: *RIKEN Genomic Sciences Center, Human Genome Research
Goroup * Institute of Molecular Biotechnology, Genome Analysis *
Kelo University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
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41578: contig of 7014 bp in length
41678: gap of unknown length
55200: contig of 13522 bp in length
55300: gap of unknown length
89559: contig of 34359 bp in,length
89559: contig of 34359 bp in,length
155919: contig of 66160 bp in length
156019: gap of unknown length
156019: contig of 108503 bp in length
contig of 6889 bp in length
gap of unknown length
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AL163302 AP001757 BA000005
AL163302.2 GI:7717445
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* e.mail: gscj-submit@genome.imb-jena.de

* URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                1. .264522
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                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="rp23-11f20"
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                    * Keio University School of Medicine, Dept. of Molecular Biology, *
Tokyo 160-8582, Japan,
* e.mail: shimizu@dmb-med.keio.ac.jp
* URL: http://adenine.dmb.med.keio.ac.jp/
                                                                                                                              GBF, Dept. of Genome Analysis,
Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
                                                                                                                                                                                                                         * Max-Planck Institute for Molecular Genetics,

* Ihnestrasse 73, D-14195 Berlin, Germany,

* e.mail: info-chr21@nengg.de

* URL: http://chr21.rz-berlin.mpg.de/.

Location/Qualifiers

1. 340000

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10026 10210
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Martinez, M.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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Homo sapiens, clone MGC:45023 IMAGE:4177041, mRNA, complete cds.
BC033766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc_mgc@hngri.nin,gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,F.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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Young,A., Zhang,L.-H. and Green,E.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1050)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/
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Pred. No. 2;
0; Mismatches 0; Indels 0.
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15873. .16018
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Email: cgapbs-r@mail.nih.gov
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100.0%; Pre
0; }
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Best Local Similarity 100.
Matches 22; Conservative
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VERSION
KEYWORDS
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BC033766
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANIZODIUM leguminosarum bv. viciae plasmid pRL6JI fixA,B,C, & W AJ431175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulación simblotica de la expresion del sistema hidrogenasa por NifA en R. leguminosarum bv. viciae Thesis (2000) Department of Biotecnologia, Universidad Politecnica
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Submitted (14-FEB-2002) Martinez M., Biotecnologia, ETSI Agronomos
Uni. Politecnica Madrid, Ciudad Universitaria s/n, Madrid, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ431175.1 GI:18857702

deltaNifH gene; fixA gene; fixB gene; fixC gene; fixW gene; ORF5;
ORF71; ORF79.

Rhizobium leguminosarum bv. viciae.

Rhizobium leguminosarum bv. viciae

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Autoregulation of nifA in symbiois of Rhizobium leguminosarum bv.
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/organism="Rhizobium leguminosarum bv. viciae"
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Pred. No. 7.2;
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PRI 01-JAN-1997 ,
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1398 c 1463 q 1050 t
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100.0%;
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4241. .5061
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                                                                                                                                                                                                                                                                                                                                                                                                            LTSHGNR'
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Best Local Similarity
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                                                                              promoter
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HSU22027/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="YFX2 protein"
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FDHSGEMDEDWLKASLSFHVPKTFVVDRDGSIAFIGDLVMLQDVLPKVIDGTWRASAE
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                                                                                                                                                             959. .961 /note="Nifa binding site (UAS)" 972. .974
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1515. .2072
                                                                                                complement(399. .401)
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                                                                                                                                                                                                                     372, 974
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                      /note="ribosome" binding site"
complement(299. .312)
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/transl_table=11
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/transl_table=11
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1267. .1506
/note="ORF79"
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1107, 1202
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1092. .1095
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//note="ORF71"
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/gene="fixW"
1525. .1527
/gene="fixW"
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/gene="fixW"
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Gaps

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1.1%; Score 21; DB 9; Length 7215;
100.0%; Pred. No. 7.4;
Live 0; Mismatches 0; Indels
                                                                                       1634 GGGCAGAGAGAGGCAGGGAGG 1654
                                                                                                         AR069321.1 GI:7220209
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                                                              Conservative
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                                                                                                                                                                                                                                                                         unidentified.
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                              Query Match
Best Local Similarity
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A47885/c
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JOURNAL
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4257. .4398,4873. .5060,5577. .5718,6308. .6489)
/gene="CYP2A6V2"
                                                       Eukaryoffa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 7213)
Fernandez-Salguero, P., Hoffman, S.M., Cholerton, S., Mohrenweiser, H., Rautio, H., Rautio, A., Pelkonen, O., Huang, J.D., Evans, W.E., Idle, J.R. et al.

A genetic polymorphism in coumarin 7-hydroxylation: sequence of the human CYP2A genes and identification of variant CYP2A6 alleles Am. J. Hum. Genet. 57 (3), 651-660 (1995)
                                                                                                                                                                                                                      2 (bases 1 to 7215)
Pernandez-Salguero, P.
Pirandez-Salguero, P.
Submitted (01-Mar.1995) Pedro Fernandez-Salguero, National
Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20894, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="cytochrome p450"
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EQATFDWVFRGYGVYFSNGERAKQLLRFAILTLRDFCVGKRGIEERIQEESGFLIEAI
RSTHGANIDPTFFLSRTVSNVISSIVFGDRFDYRDKEFLSLLRMMLGIFOFTSTSTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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/gene="CYP2A6V2"
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 U22027.1 GI:1008461
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                              Homo sapiens.
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PAT 07-MAR-1997
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1.1%; Score 21; DB 6; Length 7216;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 21; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.4;
Live 0; Mismatches
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                                                                                                                                                                                         US HEALTH (US)
Other publication AU 2860295 960105.
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                                                                                                                                       Gonzalez, F. J. (Alla, J.R.)
DEFECTS IN DRUG METABOLISM
Patent: WO 9534679-A 3 21-DEC-1995;
US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 7216)
Gonzalez,F.J. and Idle,J.R.
Defects in drug metabolism
Patent: US 5891633-A 3 06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3 from patent US 5891633.
Sequence 3 from Patent W09534679.
                                                                                                                                                                                                                                         1. .7216 /organism="unidentified"
                                                                                                                                                                                                                                                                          /db_xref="taxon:32644"
2196 c 1746 g 1
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2196 c 1746 q
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HSU22028/c

SOURCE

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PAT 18-FEB-2000
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1.1%; Score 21; DB 9; Length 8778;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 21; Conservative 0; Mismatches 0; Indels
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tive 0; Mismatches
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2663 c 2015 g 2071 t
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Gonzalez,F.J. and Idle,J.R.
Defects in drug metabolism
Patent: US 5891633-A 4 06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other publication AU 2860295 960105.
Location/Qualifiers
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Gonzalez,F.J. and Idle,J.R.
DEFECTS IN DRUG METABOLISM
Patent: WO 9534679-A 4 21-DEC-1995;
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Sequence 4 from patent US 5891633.
AR069322
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Sequence 4 from Patent WO9534679.
A47886
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1. .8779
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2663 c 2015 q
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2663 c
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join(661. .840,1117. .1279,2232. .2381,2590. .2750,3917. .4093,
5813. .5954,6440. .6627,7155. .7296,7956. .8137)
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/product-"cytochrome P450"
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ROATFDWILFRGYGYNSNVISSIVFGDREDXEBLEILLENAMIGREOFTGTSTGO
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EBEKNPNTEFYLKNLVWTTLNLFFAGTETVSTTLRYGFILLMKHPBYBEAKVBEBIDRY
IGKNROPKFEDRAMPYTEAVIHEIORRGORKSARPROFFSIGRRYCFGEGLARMELF
PMLGSELRDPRFFSNPOASPGPIDVSPKHVGFATIPRNYTMSFLPR"
//DFTTLMQNFRFKSPQSPKDIDVSPKHVGFATIPRNYTMSFLPR"
                                                                                                                     Boxaryott: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 8778)

Fernandez-Salguero, P., Hoffman, S.M., Cholerton, S., Mohrenweiser, H., Raunio, H., Rautio, A., Pelkonen, O., Huang, J.D., Evans, W.E., Idle, J.R. et al.

A genetic polymorphism in coumarin 7-hydroxylation: sequence of the human CYP2A genes and identification of variant CYP2A6 alleles
Am. J. Hum. Genet. 57 (3), 651-660 (1995)
                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-MAR-1995) Pedro Fernandez-Salguero, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20894, USA On Jan 14, 1997 this sequence version replaced gi:1008463.

1. Coation/Qualifiers
1. 8778
         PRI 01-JAN-1997
HSU22028 8778 bp DNA linear Human cytochrome P450 (CYP2Al3) gene, complete cds. U22028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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5813. .5954
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/gene="CYP2A13"
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Fernandez-Salguero, P.
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2232. .238
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PRI 24-MAY-2001

HSDJ127L3 73198 bp DNA linear PRI 24-N Human DNA sequence from clone RPI-127L3 on chromosome llpl3

HSDJ127L3/c DEFINITION

Contains GSSs and STSs, complete sequence. AL096793

AL096793.20 GI:10432580

ACCESSION

VERSION

Homo sapiens

ORGANISM

KEYWORDS

human.

Frankland, J.

AUTHORS REFERENCE

JOURNAL

COMMENT

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT: Tr:, TREMBL; WP:, WORMPEP: Information on the WORMPEP database can be found at
                                                              AL807743 30826 bp DNA linear PRI 18\text{-}JUL\text{-}2002 Human DNA sequence from clone RPl1-1047H1 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/ChrX
RPI1-1047H1 is from the library RPCI-11.4 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (18-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 19, 2002 this sequence version replaced gi:21694492.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute
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100.0%; Pred. No. 7.6;
tive 0; Mismatches
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VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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6286 c 6465 g 8'
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RESULT 45
AL807743
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                                                                                                                                                                                                                                                        SOURCE
```

Submitted (29-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, Calo Lish, Wr. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonereques@sanger.ac.uk Clone requests: clonereques@sanger.ac.uk Clone Sep 29, 2000 this sequence version replaced gi:10178889.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with the following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 73198)

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone RPI-12713 It may be shorter because we sequence overlapping sections only once, except

```
Since the because we sequence overlapping sections only once, exception a 100 base overlap.

The true left end of clone RPI-69B10 is at 73099 in this sequence. The true right end of clone RPI-181.72 is at 100 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is an annotation using the 'unsure' feature key. This sequence was generated by the Sanger Centre from a human chromosome 11 bacterial clone contig constructed by Niederfuhr A. Hummerich H, Gawin B, Boyle S, Little PF, Gessler M. Genomics 1998 oct 15;53(2):155-63

RPI-12713 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .700
/note="LIMA3 repeat: matches 5524. .6214 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="L1MA3 repeat: matches 6214. .6294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1M2 repeat: matches 1555. .1830 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="FLAM_A repeat: matches 1. .100 of consensus"
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/note="L1PA3 repeat: matches 1. .3637 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3681. .3909
/note="SVA repeat: matches 3. .231 of consensus"
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hote="26 copies 2 mer ta 86% conserved"

1391. 3680

hote="LiPpA repeat: matches 3636. 5925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="p13"
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0;

Gaps

0;

0; Indels

RESULT 46

Conservative

21;

Matches

QY

Best Local Similarity

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7056-"LiPAlO repeat: matches 5439. .6159 of consensus."
7061-"LiPAlO repeat: matches 5439. .6159 of consensus."
706-"LiPAlO repeat: matches 6481. .6493 of consensus."
706-"AluSx repeat: matches 1. .309 of consensus."
706-"AluSx repeat: matches 6493. .6911 of consensus."
70078. .10365.
7004-"AluSo repeat: matches 1. .289 of consensus."
7006-"AluSo repeat: matches 6911. .7005 of consensus."
7006-"LiMC4 repeat: matches 6911. .7005 of consensus."
7004-"AluSg1 repeat: matches 1. .297 of consensus."
7004-"LiMC4 repeat: matches 7005. .7234 of consensus."
7004-"LiMC4 repeat: matches 7078. .7523 of consensus."
7004-"LiMC4 repeat: matches 7078. .7523 of consensus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note="Limids repeat: matches 7078. .7523 of consensus" 11373. .11811

// note="Limids repeat: matches 2572. .3021 of consensus" 11798. .12026
// note="Limid repeat: matches 1239. .1464 of consensus" 12863. .13196
// note="match: GSs: Em:Aq488953" / 1562
// note="match: GSs: Em:Aq488953" / 15562
// note="match: GSs: Em:Aq488953" / 15562
// note="match: GSs: Em:Aq488953" / 15562
// note="match: GSs: Em:Aq151486" / 16736 of consensus" / 16738 / 16738 / 16738 / 16738 / 16738 / 16738 / 16738 / 16738 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 16736 / 
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/note="15 copies 2 mer gt 96% conserved"
/note="15 copies 2 mer gt 96% conserved"
/note="MBE58B repeat: matches 37. .340 of consensus"
25771. .26172
/note="Link7 repeat: matches 5892. .6287 of consensus"
26495. .27088
/note="match: GSS: Em:AQ077155"
26585. .27514
/note="LineBarepeat: matches 5090. .6136 of consensus"
27513. .28739
/note="LineBarepeat: matches 2512. .3729 of consensus"
28740. .20940
                                          .6481 of consensus"
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7937. .8595
/note="L1MC4 repeat: matches 5852.
   repeat_region
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95359 bp DNA linear PRI 17-JUL-2002
Homo sapiens chromosome 17, clone RP11-1084K4, complete sequence.
AC078903
AC078903.11 GI:21886885
HTG.
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Anote="LiMC4 repeat: matches 7516. .7587 of consensus"
40596. 40860

Anote="AluSx repeat: matches 44. .309 of consensus"
40611. 41191

Anote="LiMC4 repeat: matches 7587. .7888 of consensus"
Anote="LiMC4 repeat: matches 7587. .7888 of consensus"
Alione="AluSy repeat: matches 1. .250 of consensus"
Anote="AluSy repeat: matches 1. .258 of consensus"
Anote="AluSy repeat: matches 1. .288 of consensus"
Alione="AluSy repeat: matches 1. .288 of consensus"
Alione="AluSx repeat: matches 3. .297 of consensus"
Alione="AluSx repeat: matches 3. .297 of consensus"
Anote="AluSx repeat: matches 6004. .6141 of consensus"
Anote="LiPA6 repeat: matches 5004. .6141 of consensus"
Anote="LiPA6 repeat: matches 3614. .4523 of consensus"
Anote="LiPA6 repeat: matches 3614. .4523 of consensus"
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/note="MER52A repeat: matches 1. .1755 of consensus" 3437 //note="MAL repeat: matches 1500. .1583 of consensus" 34949. .35236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                 /note="AluSg repeat: matches 1. .286 of consensus" 36628. .36916
/note="AluJo repeat: matches 1. .304 of consensus" 37182. .37309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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L00.0%; Pred. No. 7.7;
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/note="match: GSS: Em:AQ812912"
complement(44812, 45231)
/note="match: GSS: Em:AQ337862
match: STS: Em:G60966"
complement(44836, 45296)
/note="match: GSS: Em:AQ821283"
complement(44839, 45293)
/note="match: GSS: Em:AQ831283"
45147, 45216
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Matches 21)
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AC078903
LOCUS
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VERSION
KEYWORDS
SOURCE
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ORGANISM

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

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complement(9706. .9748)
/rpt_family="L2"
10777. .10817
/rpt_family="CT-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="AluSp"
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/rpt_family="(T)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L2"
2494. .2606
/rpt_family="MIR"
3458. .3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /22. .830
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1337. 1362
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                                                                                                                                              With Distribution of the Control of 
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 95359) Birran, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-1084K4 Unpublished
  Homo sapiens
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TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

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T7 end overlaps AC020558 [WashU]; we are submitting only the first 95.4 kilobases of the project.

Location/Qualifiers
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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complement(2372. .2485)
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Center clone name: 1084_K_4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family="MLT1J2"
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125. .5436
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Sus scrofa clone XX-339A5, *** SEQUENCING IN PROGRESS ***, 4
2 (bases 1 to 105448)
DOE Joint Genome Institute.
Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                           Submitted (1997-FBB-2000) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA (bare) 1 to 105448)

Dob Joint Genome Institute and Stanford Human Genome Center. Direct Submission
Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA (color by 2000 this sequence version replaced gi:6938856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (Sabra, H. Subnission Direct Subnission Subnistted (14-ANG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 19, 2002 this sequence version replaced gi:21911701.
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                                                                                           3 (bases 1 to 105448) \, DOE Joint Genome Institute and Stanford Human Genome Center.
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                   www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                     www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .105448
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                                                                                                                               Direct Submission
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 105448)
Dob Joint Genome Institute and Stanford Human Genome Center.
Unpublished
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100.0%; Pred. No. 7.7;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 21; Conservative
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AC010494
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AL773562 126895 bp DNA linear HTG 16-AUG-2002
Sus scrofa clone XX-649D6, *** SEQUENCING IN PROGRESS ***, 2
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                               Quality coverage: 9.65x in Q20 basés; sum-of-contigs Quality coverage: 10.29x in Q20 bases; agarose-fp
                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gap between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 21; DB 2; Length 119707; 100.0%; Pred. No. 7.7; 1ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                   2907 3006: gap of 100 bp 100 bp 24104 24203; contig of 21097 bp in length 24204 73965; contig of 49762 bp in length 73966 74065; gap of 100 bp 74066 119707; contig of 45642 bp in length Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           be preserved.

1 2906: contig of 2906 bp in length
Consensus quality: 118859 bases at least Q40 Consensus quality: 119194 bases at least Q30 Consensus quality: 119151 bases at least Q20 Insert size: 119407; sum-of-contigs Insert size: 117704; 8.6% error; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .2906
/note="assembly_fragment:01782"
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/note="assembly_fragment:01878"
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/note="assembly_fragment:02763"
. 27491 c 27653 g 31695 t ::
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/note="assembly_fragment:01931"
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="Xx-339A5"
/clone_lib="SBAB"
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Best Local Similarity 100.C
Matches 21; Conservative
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Gaps
                                                      Assembly program: XARPA; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator: 13% of reads
Chemistry: Dye-terminator Big Dye; 86% of reads
Consensus quality: 126469 bases at least Q40
Consensus quality: 126617 bases at least Q20
Insert size: 126795; sum-of-contigs
Insert size: 126795; sum-of-contigs
Quality coverage: 9.62x in Q20 bases; sum-of-contigs Quality
Coverage: 10.33x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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1. 53711
/note="assembly_fragment:00021
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100.0%; Pred. No. 7.7
Live 0; Mismatches
Project Information
                                          --- Summary Statistics
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/clone="xx-649D6"
                     Center project name: bS649D6
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December 28, 2002, 16:45:43; Search time 1771.2 Seconds (without alignments) 12124.644 Million cell updates/sec
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1 atgctgcatccagagacctc......gaaaccgttacatctgccag 1326
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          OM nucleic - nucleic search, using sw model
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	Description	BI764403 603046141	BM924615 AGENCOURT	BI517774 603042018	BM547887 AGENCOURT	BI760121 603044615	BI757380 603029310
SUMMARIES	ID	.BI764403	BM924615	BI517774	BM547887	BI760121	BI757380
	DB	13	14	13	13	13	13
	Length	836	1034	928	1076	710	939
dФ	Query ore Match Length DB I	56.9	56.7	54.6	51.6	51.0	47.7
	Score	754	752.2	723.4	684.6	929	632.2
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UI - E DKFZF 603C 603C	2480 2480 6030			BI75735 603045609 BM481198 533084 MA BF078053 228296 MA BF577554 602040477 AW314352 10382 MAR BB496538 BB496538 BI134777 UT-M-BH3- BQ720124 AGENCOURT BH327544 CH330-105	AW465507 BP230019B BI976862 486025 MA BM708158 UT-E-CII- AI989724 W35502.x AI627475 ty80a06.x AI433291 ti86b01.x AW433675 77432 MAR AW001740 W804c06.x BH040326 RPCI-24-3
BM695392 AL040183 BI759120 BI759353	AI792411 BF198258 BI761101 BT340175	BGL5401/5 BGG08968 BI775946 AW437073 BB602462 BI359591	A1307814 AW786132 BF057185 AW299257 BQ006636 BQ446805	B1759735 BN481198 BN481198 BF527554 AW314352 BB496358 B113477 B113477 BH327544	AW465507 B1976862 B1976862 A1989724 A1627475 A1433291 AW436875 AW001740 BH040326
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ALIGNMENTS

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                                                                    /ntole="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NoII; Site_2: ECCRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (ECCRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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Pred. No. 1.9e-159;
                                                                                                                                                                                                                                                                                                                       0; Mismatches
                         /clone="IMAGE:5186219"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                         Query Match 56.9%;
Best Local Similarity 97.7%;
Matches 807; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                             CTGGCTCAAGCCAGGCCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG
                                                                                                                                                                 CTGGCTCAAGCCAGGCCACCTCTGTGGAACCCCAACCCCGAGCCTGGCGTCCGGCCTG
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Itssue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                        TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGCGGGGGTTGGCGTCCTTT
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                                                                                                                           /note="Organ: pooled colon, kidney, stomach; vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 3 stomachs, 62 yo male and 70 yo female. Library is oligo-dr prined and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size rows cloning. Average insert size and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NHLMGC Library."
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94.9%; Pred. No. 1.6e-152;
tive 0; Mismatches 36;
                             1. 928
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/clone="IMAGE:5182397"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
High quality sequence stop: 860
Location/Qualifiers
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                                                                                                                                                                                         BM547887 1076 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633
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                               782 ACGICICAACAICAG-ACCIGGCACIGGCACIGICCCCCIGIGIAACACGGCAGAIACIG 840
                                                                     61 CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC 120
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                                                          GCCAAGTGAGGTGCAGCCTGCAGTG-TGTGCACGGCCGGTTCCGGGA--GGAGGAGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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/tissue_type="hippocampus"
/lab_host="DH108"
                                                                                                       836 CGTGCGTCTGTGACATCGGCTACGGGG 862
                                                                                                                                 CAGGGGTCTGGGAACATCGGAACGGGG 927
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JOURNAL
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KEYWORDS
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BI760121 710 bp mRNA linear EST 25-SEP-2001 603044615F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5184962 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 710)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                              CTGGGCTGTGGGCGGCACCTGTGCTGTGCAGGCCAGCGATAGAAGCCTTTGTCTGT
376 GGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCTCCCTGCAACCGCCTGCGCAGC
                                                                   TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA
                                                                                                                                                                                                CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG
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Mon Dec 30 09:16:19 2002

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BI757380 939 bp mRNA linear EST 25-SEP-2001 603029310F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5199674 5',
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/clone_lib="NIH_MGC_114"
/clone_lib="NIH_MGC_114"
/lab_host="Hil08"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI: Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-7 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb, Library is normalized and enriched for
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 939)
NIH-WGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M. A.G.E. Consortium (LLNL)
DNA Sequencing by: They Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga.llnl.gov.column: 03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 ATGCTGCATCCACAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.7%; Score 632.2; DB 13; Length 939; 96.1%; Pred. No. 5.5e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Indels
666 CCACTGTCCCCTGGCTACACGGGGCAGATACTGCCAAGTGAGG 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                    CMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 colons, 40 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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228 c 226 g 125 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 676; DB 13;
Pred. No. 6.7e-142;
0; Mismatches 10;
  http://image.llnl.gov
Plate: LLAM11461 row: n column: 03
                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5184962"
                                                                                                                                                                          /clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                            High quality sequence stop: 704.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.0%;
98.4%;
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UI-E-CQ1 is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a NOT I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCMTMAAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 bp mRNA linear EST 29-FEB-2000 onym: htes3) Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1070 ACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCAACAAGA 1129
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0
                                                                                                                                                                                                                                                                                                                                                               46.9%; Score 622.2; DB 14; Length 645; 99.5%; Pred. No. 8.5e-130; Live 0; Mismatches 3; Indels 0;
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DKF2p434F2413_r1 434 (synonym: h<sup>1</sup>
DKFZp434F2413 5', mRNA sequence.
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AL040183.1 GI:5409148
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/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/net_bost="bH10B (Life Technologies) (Tl phage resistant)"
/note="Organ: egy; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Lowa (1970) and mapping (1970) and mapping (1971) and mapping (1971) and mapping (1971) and mapping (1971) and medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9856
Email: msoares@blue.weeg.uiowa.edu
Tissue Produrement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa Clana Distribution: Researchers may obtain clones from Research Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 645)
Bonaldo,M.E., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                             TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGGCTTGGCGTCCTTT
                                                                                                     GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAG
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UI-E-CQ1-aev-n-19-0-UI.rl UI-E-CQ1 Homo sapiens cDNA clone
UI-E-CQ1-aev-n-19-0-UI 5', mRNA sequence.
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/clone_lib="UI-E-CQ1"
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                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DFK2); Email s.wiemann@dkfz- heidelberg.de;
Sequenced by BMFZ (Blomedical Research Center at the Charite,
Berlin/Germany) within the CDNA sequencing consortium of the German
                          Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 704)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. Est (Koehrer, et al.)

Unpublished (1999)

Contact: Koehrer K.
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                                                                                                                                                                                                                                                                                                      sī sequence also available.
This clone (DKFZp434F2413) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGGAGGTGCCTGGTGTTCGCTCTGCACCAGTGTCTCATGCTGCTGCTTCAAAGCCTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 579.8; DB 9; Length 704; Pred. No. 3.1e-120; 0; Mismatches 13; Indels 7
                                                                                                                                                                                                                                                                                                                                                         Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434F2413"
/clone=lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector:
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97.18;
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/ncce="Occurred to the color, kidney, stomach; Vector: pcWv-SPORT6; Site_1: NotI; Site_2: ECGRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally choned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI759120 709 bp mRNA linear EST 25-SEP-2001 603042530F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182999 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
NIH-WCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11456 row: 1 column: 08
High quality sequence stop: 709.
Location/Qualifiers
1.709
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                                                                                                                                       538 AGGTGATTGACAGTGACTTCTAGACCA-GAACTTCTGGATCGGGCTCACCTACAAGACCG 596
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478 GAGCCACAAAGTGCAANGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACG 537
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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BI759353 916 bp mRNA linear EST 25-SEP-2001 603043013F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183330 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA 240
                                                                                                  230 CTTGGCACCGCCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC 289
                                                                                                                                          CTGGCTCAAGCCAGGCCAGCCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG 300
                                                                                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 916)
NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                         TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCCTTT
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Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LENL at:
http://inage.llni.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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Location/Qualifiers
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BI759353
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852 bp mRNA linear EST 25-SEP-2001
603048444F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188643 5',
B1762690
stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code closs. Note: this is a NIH,MGC Library.
                                                                                                                                                                                                                                                                                                             117 GGCCGGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCCCTGCACAACCGCCTG-C 175
                                                                                                                                                                                                                60 CCTTG-GCACCACCTGGGCAGAGGTGTGGCCACC-CCAGCTGCA-GGAGCAGGCTCCGAT 116
                                                                                                                                                                                                                                                                                                                                                                                    CGTCCTTTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGG--CAGCGGTACAGCCACGC 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 AGCCTTTGTCTGTGCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCAT
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                                                                                                                                             DB 13; Length 916;
                                                                                                                                                                          57; Indels
                                                                                                                                             36.9%; Score 489.8; DB 13 90.5%; Pred. No. 6.5e-100;
                                                                                                                                                                       0; Mismatches
                                                                                                                                                          Local Similarity 90.53 tes 701; Conservative
                                                                                                                                             Query Match
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yo of 2

/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2

418 GAGTGTGGTACGCCACCTGCACCCACTACA-CGCAGCTCGTGGGGCCACCTCAAG 476

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/db_xxef="taxon:9606"
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/clone="IMAGE:5188643"
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/clone="IMAGE:116"
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/note="Organ: pooled colon, kidney, stomach; Vector:
pcMv-SPORT6; Site_1: NotI; Site_2: EccRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 5
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH,MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imag-llnl.gow g column: 12
Plate: LLAM11471 row: g column: 12
High quality sequence stop: 849.
Location/Qualifiers
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                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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  BI762690.1 GI:15754256
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Best Local Similarity
                                                              Homo sapiens
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/sex="pooled (6)"
/lab_host="pooled (6)"
/lab_host="religion"
/lab_host=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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This 5' resequenced clone has no previous 5' data to verify this
477 CCAGCTGGGCTGTGGGCGGCACCT--GTGCTGCAGGCCAGACAGCGATAGAAGCCTTT 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an34b09.y5 Gessler Wilms tumor Homo sapiens cDNA clone
IMAGE:1700537 5' similar to TR:043692 043692 25 KDA TRYPSIN
INHIBITOR: , mRNA sequence.
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                                                                                                                                                                                                                                                                          /clone="IMAGE:1700537"
/clone_lib="Gessler Wilms tumor"
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/db_xref="taxon:9606"
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High quality sequence stop: 429.
Location/Qualifiers
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AI792411.1 GI:5340127
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 429)
Fahrenkrug's.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                   EST 03-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine functional formula for the contact: Smith TPL Contact: Smith TPL USDA, ARS, US Meat Animal Research Center Fals, 402 762 4366 Fax: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pcMv SPORT6; Site_1: Not1: Site_2: Sal1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 125 c 182 g 85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   838 TGCGTCTGTGACATCGGCTACGGGGAGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTC 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA 240
                                                                                                                                                          CIGGCICAAGCCAGGCAGCCCICIGIGGAAICCCAACCCCGAGCCIGGCAICCGGCCIG
                                                                                                                                                                                                                              CITEGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 313.4; DB 12; Length 429; Pred. No. 2.6e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                248012 WARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF198258
                                                                                                                                                                                                                                                                          301 TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGC 357 460
                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                  427 TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                           429 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 78 row: B column: 9
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
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84.8%;
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Best Local Similarity
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BF198258
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/clone_lib="NHM_MGC_lib"
/lab_host="NHM_MGC_lib"
/lab_host="DHi0B"
/note="Organ: pooled colon, kidney, stomach; Vector:
/note="Organ: pooled colon, kidney, stomach; Vector:
pcMv-SpORT6; Site_l: Not!; Site_l: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI761101 500 bp mRNA linear EST 25-SEP-2001 603043573F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183898 5', mRNA sequence.
BI761101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.go.

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.go.

Plate: LLAM11459 row: a column: 19
                                                                                                                                                                                                                                                                                                                                                                                               GACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198 CCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAG 1257
                                                                                                                                                                                              1078 ACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAG 1137
                                                                                                958 TATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGC 1017
                                                                                                                                                                                                                                                                                                                        361 CCTGACAACCA-------GGGCTTTGGCAACTGTGTGGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 500)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                       898 CACACCIGIGACCIGAGGAICGACGGAGACIGCTICAIGGIGICTICAGAGGCAGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1258 CTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCA 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 CTGCAGGCATCGGCCGCTTCAACTGGAATGATCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 480.
Location/Qualifiers
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BI761101
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
FORMARD: AGGAAACAGCTATGACCAT
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Fahrenkrug-K.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library." 180~c~151~g~85~t
                                                                                                                                 316
                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                  181 TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA 240
                                                                                                                                                                                                                                                                                                                                    241 CTGGCTCAAGCCAGGGCAGCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCC-T 299
                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                               CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC
                                                                                                                                                                                                                                                                         GGAGCCCTGAACAGGAAGGAGGTTCTTGCTCCTCCTCCTGCACAACCGCCTGCGCAGC
                                                                           Score 299.4; DB 13; Length 500;
Pred. No. 4e-57;
0; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365365 MARC 2PIG Sus scrofa cDNA 5', mRNA linear B1340175. G1:15033458 EST.
                                                                                                         6; Indels
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/db_xref="taxon:9823"
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/tissue_type="pooled"
/lab_host="DH10B"
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Plate: 104 row: P column: 4
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 GTGGCGCACCCTGCAAGCTGG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                           300 GTGGCGCACCCTGCAAGTGGG 320
                                                                           22.6%;
97.8%;
                                                                                                    Matches 314; Conservative
                                                                                         Similarity
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                            84
                                                                           Query Match
                                                                                       Best Local
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                            BASE COUNT
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                                                                                                                                                                                               61
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VERSION
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BI340175
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1;
/note-"Vector: pcMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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                                                                                                                                                                                                                 97 CTGCAGG---AGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTC 153
                                                                                                                                                                                                                                                                                        154 CTCTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGG 213
                                                                                                                                                                                                                                                                                                                                                                 394 CAGCGGTACAGCCACGGGCAGGAGAGTGTGCTCGCAACGCCACCTGCACCACTACACG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                          37 CTCCTGGCTGTGCTCCTGGCCCTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAG 96
                                                                                                                                                                                                                                                                                                                                                                                                                         214 CTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 CCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTGGGGCTGGAACATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 CTGCTGCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGG
                                                                                                                                                          3,
                                                                                                                     Length 521;
                                                                                                             22.1%; Score 293.2; DB 13; Length 82.2%; Pred. No. 1e-55; ive 0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: December 28, 2002, 20:45:38 Job time: 1778.2 secs
                                                                                                                                   Best Local Similarity 82.2
Matches 350; Conservative
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 15:41:47; Search time 3382.86 Seconds

(without alignments)
11407.612 Million cell updates/sec

Title:
Perfect score: 1326
Sequence: 1 atgctgcatccagagacctc......gaaaccgttacatctgccag 1326
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Maximum Match 100%
Listing first 45 summaries

GenEmbl:*

1: 9b_ba:*
2: 9b_hig:*
3: 9b_in:*
4: 9b_pat:*
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Pred. No. is the number of results predicted by chance to have a

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         Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP) Location/Qualifiers
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                                                                                              Length 1341;
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                                                                                             94.6%; Score 1254; DB 6;
llarity 97.6%; Pred. No. 7.9e-250;
Conservative 0; Mismatches 5;
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Patent: WO 0149728-A 15 12-JUL-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1775)
Kato, S. and Kimura, T.
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                               Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP) Location/Qualifiers
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TGCTGC TGCTGC	36CA	2 GGAGCC	1 TGGGTC 2 TGGGTC	1 CTGGCT 	1 TGGCG 2 TGGCG	1 GTTGAAG 2 GTTGAAG	1 TGTGCTCG 2 TGTGCTCG	1 CTGGGCT 2 CTGGGCT	TACTC TACTC	GGTGCCTG GGTGCCTG	GCAGO	CGTCTC 	CAAGTGAG CAAGTGAG	GTCTGTGP GTCTGTGP	ACCTGTGAC ACCTGTGAC	TACAGA TACAGA	AAAGTG AAAGTG
Qy Db 6 Qy 6	Db 12	1 ਜ	Oy 18 Db 24	Qy 24. Db 30.	36	Oy 361 Db 422	4 4 8	Qy 481 Db 542	Qy 541 Db 602	Oy 601 Db 662	Qy 661 Db 722	Qy 721 Db 782	Oy 781 Db 842	Qy 841 Db 902	Qy 901 Db 962	Qy 961 Db 1022	Oy 1021 Db 1082

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Direct Submission
Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de,
Sequencing consortium of the German Genome Project. This clone
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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HOMO sapiens MRNA; CDNA DKFZp686E1934 (from clone DKFZp686E1934).
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/clone_lib="666 (synonym: hlcc3). Vector pSportl_Sfi; host
DH10B; sites Sfi1A + Sfi1B"
/dev_stage="adult"
3171. 3176
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   1141 TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCT 1200
                                                                                   1201 GACAACCACGGGCTGGTGTGGCTGGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG 1260
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Ottenwaelder, B., Obermaler, B., Mewes, H.W., Weil, B., Amid, C. and
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/db_xref="taxon:9606"
/clone="DKF2p686E1934"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                          TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGGGGCTTGGCGTCCTTT 360
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Location/Qualifiers
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AB060195 2900 bp mRNA linear PRI 13-JUN-2001
Macaca fascicularis brain cDNA clone:QccE-21387, full insert
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Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone_lib:macaque brain cDNA library QccE clone:QccE-21387.
Bukacaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                      DB 6;
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50.7%; Score 672.8; DB 6;
Best Local Similarity 99.3%; Pred. No. 2.7e-129;
Matches 685; Conservative 0; Mismatches 4;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 197 c 212 g 131
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AB060195.1 GI:13676426
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REFERENCE

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Mon Dec 30 09:16:14 2002

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Submitted (17-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URE:http://www.nih.go.jp/yoken/genebank/, Tal:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R. Sitel: Drail (ACCATGTG)
R. Sitel: Drail (ACCATGTG)
R. Sitel: Drail (ACCATGTG)
R. Sitel: Drail (ACCATGTG)
POSCIPION: Ist strand cDNA was primed with an oligo(dT) primer using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was parformed to exclude fragments 4.15kD. The Sfil digested PCR product was cloned the Drail sites of pME185-FL3. Xhoi sites just outside the Drail sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method
Signano et al., Institute of Medical Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGCGRHLCSADQAAIEAFVCAYSPGGNWEVNCKTIVPYKKGAWGSLCTASVSGCFKAW
DHAGGLCGEOMRAQSGDPGVGVAASYWAVPEAPTLSYQGGSCPACWEETLFSSSPPPL
TRGPQEPLSHELPEPRTSQHQHLPLPLSTWLHWQVLPSAVQPAVCARPVSGGGVLVRL
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TLQVGWVVQLLLPAGSASFVEVVSLWFAEGGRYSHAAGECARNATGTHYTQLVWATSSQ
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Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K. Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 Argericadarcrecerecereses and argerical argerical and argerical argerical
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Unpublished
2 (bases 1 to 2900)
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Indels 157;
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/clone_lib="macaque brain cDNA library QccE"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PME18S-FL3 (Acc.No. AB009864)
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/protein_id="BaB41141.1"
/db_xref="GI:13676427"
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0; Mismatches 42;
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Location/Qualifiers
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/clone="QccE-21387"
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PRI 04-AUG-2000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180596)
241 CTGGCTCAAGCCAGGCCAGCCCTCTGTGGAATCCCAACCCGGAGCCTGGCATCCGGCCTG 300
               GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAG 420
                                                                    TGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAG 480
                                                                                                                                                                               Homo sapiens chromosome 16 clone RP11-296110, complete sequence.
                                                                                                                                                                                                                                                                       541 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  '84 GCAGCATCCTACTGGGCTGTCCCAGAAGCCCCGACCTCAGCACCCAGGGAGGCTCCTGC 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  744 CTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTG 803
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                                                     301 TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTGGCGTCCTTT
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Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Submitted (03-AUG-1999) Mitchell Drive, Walnut Creek, CA 94598, USA
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 21, 2000 this sequence version replaced gi:7689944.
                                                                                                                                                                                                                                                                                                             Consensus quality: 156671 bases at least Q40
Consensus quality: 183548 bases at least Q30
Consensus quality: 188961 bases at least Q30
Consensus quality: 188961 bases at least Q30
Consensus quality: 1889610 agarcse-fp estimation
Estimated insert size: 189500; agarcse-fp estimation
Quality coverage: 3.4 in Q20 bases; agarcse-fp estimation
Quality coverage: 3.23 in Q20 bases; sum-of-contigs estimation.
Quality coverage: 3.3 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* consists of 60 content order in this sequence record is
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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28: gap of unknown length
55: contig of 1007 bp in length
65: gap of unknown length
69: contig of 1004 bp in length
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 205044)
                                                       Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 180596)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                          Direct Submission
Submitted (04-AUG-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 4, 2000 this sequence version replaced gi:9256118.
Draft Sequence Produced by DOE Joint Genome Institute
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.9% of Sequence;
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ACCO90553 153427 bp DNA linear PRI 27-JUL-2001 Homo sapiens chromosome 16 clone RPI1-252A24, complete sequence.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 163427)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (27-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 27, 2001 this sequence version replaced gi:9256116.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 CIGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATC 273
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15 150305: contig of 13791 bp in length of 150405: gap of unknown length of 15392: contig of 13587 bp in length of 14092: gap of unknown length of 186975: contig of 22883 bp in length of 187075: gap of unknown length of 205044: contig of 17969 bp in length.
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45103 c 45331 g 53992 t 5987 others
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/db_xref="taxon:9606"
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/clone="RP11-492H8"
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-572F4"
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DOE Joint Genome Institute.
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AC126771.1 GI:21717140
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Best Local Similarity 89.1%
Matches 269; Conservative
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 177479)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                       www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
ouality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
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/clone="RP11-252A24"
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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SHGC-32146 G27136
SHGC-36058 G30050.
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Direct Submission
Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197460)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY 394 CAGGGGTACAGCCACGCGGCAGAGAGTGTGCTCGCAACGCCACCTGCACCCACTACACG 453
Db 135167 CAGCGGTACAGCCACGCGGCAGAGAGTGTGCTCGCAACGCCACTGCACCACTACACG 135226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY 274 CCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTGGGCTGGAACATGCAG 333
Db 135047 CCAACCCGAGCCTGGCGTCGGCCTGTGGCGACCTGCAAGTGGGCTGGAACATGCAG 135106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 135227 caggrangrangergengergangergecangergecangercecangaracangaetrecanger 135286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 134987 CAGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGGCCAGGCAGCCCTCTGTGGAATC 135046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 135107 CTGCTGCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCACCTGTGGTTGCAGAGGGG 135166
Submitted (28-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Feb 28, 2002 this sequence version replaced gi:18071320. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC126771 197460 bp DNA linear HTG 09-JUL-2
Homo sapiens chromosome 16 clone RP11-396D24, *** SEQUENCING IN
PROGRESS ***, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 CAGCT-CGTGTGGGCCACCTCAAGCCAGCTGGGGCGGCGGCGCCCTGTGCTCTGCAGG 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 CIGGACIGGAGIGACAGCCIGGCCCAACIGGCICAAGCCAGGGCAGCCCICIGIGGAAIC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 177479;
                                                                                                                                             www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
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0; Mismatches 32;
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chimpanzee.
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Consensus quality: 193703 bases at least 030
Consensus quality: 194840 bases at least 020
Estimated insert size: 196560; sum-of-contigs estimation
Estimated insert size: 196560; sum-of-contigs estimation
Quality coverage: 2.1474836E7 in 020 bases; null estimation
* NOTE: This is a working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
* consists of the contigs of the pieces of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 125634 CAGGACTGGAGTGACACCTGGCCCAACTGGCTCAAGCCAGGGCACCCTCTGTGGAATC 125693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 125754 CTGCTGCCGCGGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTGTGGTTTGCAGAGGG 125813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 125814 CAGCGGTACAGCCACGCGGCAGCAGAGAGTGTGCTCGCAACGCCACCTGCACCCACTACACGC 125873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 CTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 CIGGIGCCCGGGGCITGGCGTCCTTTGITGAAGTGGTCAGCCIATGGTTTGCAGGGGG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 CAGCGGTACAGCCACGCGGCAGGAGGTGTGCTCGCAACGCCACCTGCACCCACTACACG 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * arbitrary. Games between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.0%; Score 238.8; DB 2; Length 197460; 89.1%; Pred. No. 1.3e-39; tive 0; Mismatches 32; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI human BAC library 11" 50025 a 47482 c 47491 g 51562 t 900 others
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gap of unknown length
contig of 19736 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 23317 bp in length
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of 23383 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1700: gap of unknown length
3466: contig of 1766 bp in length
3566: gap of unknown length
5709: contig of 2143 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown length
contig of 1991 bp in length
gap of unknown length
contig of 6827 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1600: contig of 1600 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
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gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length
                                                                                                                       Center clone name: RPCI-11_396D24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .197460
/organism="Homo sapiens"
/db_xref="taxon:9606"
Web site: http://www.jgi.doe.gov
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                                                                                       Center Project Name: 558525
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contig
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                                                          Project Information
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Remanalish Euthernals Primates; Catarrhin; Hominidae; Pan.

Mammalish Euthernals; Primates; Catarrhin; Hominidae; Pan.

Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsonok, S.L., Amaratunge, H.C., Are'J.R., Agle, M., Banks, T., Barbcooks, S.L., Amaratunge, H.C., Are'J.R., Agle, M., Bornin, D., Barbooks, S. Brieva, M., Brown, E., Brown, M., Brown, M., Brown, E., Brown, M., C., Carron, T., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chan, C., Covie, M.D., Dathorne, S.R., David, R., Earnhart, C., Edgar, D., Elago, M., Ford, J., Poster, P., Frantz, P., Ganeli, J., Garcia, A., Garner, T., Garza, M., Gill, R., Garlis, R., Harth, M., Garner, P., Hale, S., Hamilton, K., Harnandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Hollet, S., Haves, A., Hernandez, O., Hodgson, A., Hogues, M., Hollet, S., Joudah, S., Katavid, J., Liu, W., Louise, M., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinale, M., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinale, M., Massey, E., Mawhiney, E., Martin, R., Martin, C., Mine, G., Miner, C., Mitchell, T., Morken, O., Sodergren, S., Soctt, G., Sparks, A., Stanley, H., Stono, H., Savery, G., Scherer, S., Soctt, G., Sparks, A., Stanley, H., Stono, H., Savery, G., Sodergren, R., Roilbock, A., Tameria, A., Tameria, A., Tameria, A., Tameria, A., Tameria, C., Wut, Y., Wut, Y., Wut, Y., Wut, Y., Wuter, W., Williams, G., Walliams, G., Walliams, G., Walliams, C., Wut, Y., Wut, Y., Wuter, W
                                                                                                                                                                                                                                                                                                                                                                                                  HTG 22-JUN-2002
Db 125874 CAGGIGAGIGIGCIGCAGGIGAGGCCAGCGIGCCAGCTCCCAGAIACAGACTICCACIGG 125933
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Direct Submission
Submitted (14-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan,
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Submitted (22-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                    AC097331
Pan troglodytes clone RP43-53A2, WORKING DRAFT SEQUENCE, 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC097331.4 GI:21535856
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                                                                                                                                                                                                                                                                                                                                                                                                                                             unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                 Sequencing vector: Plasmid; M77789
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 190821 bases at least 040
Consensus quality: 190821 bases at least 030
Consensus quality: 193089 bases at least 030
Estimated insert size: 212811; sum-of-contigs estimation
Quality coverage: 0.x in Q20 bases; agarose-fp estimation
Quality coverage: 9.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 GGAGGCTGGACTGGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTG 268
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Baylor Plaza, Houston, TX 77030, USA
On Jun 21, 2002 this sequence version replaced gi:21450389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap to the control of 12707 bp in length contig of 12707 bp in length contig of 10083 bp in length contig of 10898 bp in length contig of 2153 bp in length contig of 2153 bp in length gap of unknown length contig of 2247 bp in length contig of 2047 bp in length contig of 2047 bp in length contig of 2043 bp in length
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                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                     Center: Baylor College of Medicine
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                                                                                                                                                              Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                       Center clone name: RP43-53A2
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Best Local Similarity
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                                                 COMMENT
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Db 177595 GGCCCCAGGACTGACAGCCTGGCCCAACTGGCTCAAGCCAGGCAGCCCTCTGTG 177536

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Mammalia; Butheria; Primates; Catarrinii; Hominidae; Pan.

(CER MIZOY, D.M., Addama, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Ali-osman, F.R., Barbaria, J., Banage, K., Blankenburg, K., Bonnia, D., Bouck, J., Bunage, K., Blankenburg, K., Bonnia, D., Chen, B., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burkett, C., Burrell, K.L., Byrd, N.C., Chavolin, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chavolin, P., Chowdhy, T., Christopoulos, C., Cleveland, C.D., Cox, C., Clevele, M.D., Dathorne, S.R., David, R., Dotthwalte, K.J., Draper, H., Dederich, D.A., Delaney, K.R., Delgado, O., Dathorne, S.R., David, R., Dotthwalte, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Denn, A.L., Ding, Y., Dubin, H.H., Douthwalte, K.J., Draper, H., Denn, A.L., Ding, Y., Dubin, H.H., Douthwalte, K.J., Draper, H., Esoter, P., Escotto, M., Palls, T., Ferraque, D.D., Flagg, M., Ford, J., Esoter, P., Kantz, P., Gansil, A., Gansil, M., Ganzel, M., Gill, K., Gorrell, J.H., Gorrell, J.H., Gorrell, J.H., Gorrell, J.H., Haves, M., Harnis, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Huber, J., Hullyk, S., Hume, J., Harnandez, J., Hernandez, O., Huber, J., Hullyk, S., Hume, J., Jackson, E., Macker, M., Han, U., Korat, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, Z., Lidrarge, O., Lieu, C., Liu, N., Li, Z., Lidrarge, C., Liu, Y., Li, Z., Lidrarge, C., Liu, Y., Li, Z., Lidrarge, C., Liu, Y., Maheshwari, M., Mapen, M., Mapen, M., Maper, J., Mattindale, A., Maher, G., Metzker, M., Maner, G., Maher, J., Mitchell, T., Mohabbat, K., Mei, C., Metzker, M., Maner, G., Maher, J., Pater, M., Pater, M., Pater, M., Ren, Y., Royen, N., Nickerson, E., Nasek, M., Ren, Y., Royen, R., Pater, M., Pater, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 20-0CT-2001
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 177355 ACACGCAGGTGAGTGTGCTGCAGGTGAGGCCAGCGTGCCAGCTGCCAGGTCCAGGTTCC 177296
QY 269 GAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCTGCAAGTGGGCTGGAACA 328
Db 177535 GAACCCCAACCCGAGCCTGGGCTCGGCCTGTGGCCACCTGCAAGTGGGCCTGGAACA 177476
                                                                                                                                              QY 329 TGCAGCTGCTGCCGCGGGGCTTGGTCCTTTGTTGAAGTGGTCACCTATGGTTTCCAG 388
Db 177475 TGCAGCTGCTGCCGCGGGCTTGCCGTCCTTTGTCGAAGTGGTCACCTATGGTTGCAG 177416
                                                                                                                                                                                                                                                                                                                                            Db 177415 AGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTCTCGCACGCCACTGCACCTGCACT 177356
                                                                                                                                                                                                                                                                                                        389 AGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCACTGCACCTT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 ACACGCAGCT-CGTGTGGGCCACCTCAAGCCAGCTGGGGCTGTGGGCGGCACCTGTGCTCT 507
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AC097271
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KEYWORDS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; M77789
Sequencing vector: Plasmid; M77789
Sequencing vector: Plasmid; M77789
Assembly program: Phrap; version 0.990329
Consensus quality: 202604 bases at least 040
Consensus quality: 204032 bases at least 030
Consensus quality: 205164 bases at least 030
Estimated insert size: 200344; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
Quality coverage: 9.4x in 020 bases; sum-of-contigs estimation
                                                                                            Wolley, n.c.,
Submission
Submitted (13-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.9%; Score 237.2; DB 2; Length 204182; 88.7%; Pred. No. 2.7e-39;
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52711 a 50970 c 50521 g 49254 t
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Weinstock, G. and Gibbs, R. Direct Submission Unpublished
                                                                                                                                                                                                                                                                                                                         Center project name:
                                                                 (bases 1 to 204182)
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Matches 268; Conservative
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                                                                                 Worley, K.C.
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Radmalals Eutherla; Primates; Catarrhini; Hominidae; Pan.

Mandmalals Eutherla; Primates; Catarrhini; Hominidae; Pan.

Muzny, D.M. Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Aet-J.R., Banks, T., Barbaria, J.,

Benton, J., Binage, M., Blankenburg, K., Bonin, D., Bouck, J.,

Burkett, C., Barkeht, C., Darke, J., Clavez, D., Chen, C.,

Carter, M., Cavasos, S.R., Chakeko, J., Clavez, D., Chen, G.,

Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,

Davy, Carroll, L., Dederich, D.A., Dellandy, K.R., Delgado, O.,

Denn, A.L., Dirdy, Y., Dinth, H.H., Douthwalte, K.J., Draper, H.,

Blad, C., Escottc, M., Earnhart, C., Edar, D., Edvards, C.

Flads, C., Escottc, M., Earls, A., Gao, J., Garcia, A., Garner, T.,

Garza, M., Gill, R., Gorrell, J. H., Guevara, W., Gunarden, P., Haale, S.,

Hernandez, J., Hernandez, O., Hodson, J., Garda, D., Edvards, C.,

Joudsman, E., Jacobson, B., Jalx, Y., Johnson, R., Johlows, M., Johloway, C.,

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Kovar, C., Kratovic, J., Kulray, S., Khan, U., King, L., Korvah, J.,

Kovar, C., Kratovic, J., Kulray, S., Khan, U., King, L., Korvah, J.,

Lewis, L. Li, J., Liz, Z., Litchtarge, O., Lieu, C., Liu, J., Liu, R.,

Ma, J., Maheshwari, M., Mapua, P., Martindale, A.,

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Matinez, E., Massey, E., Manhiney, E., McLeo, M. Pacca, M., Pave, M., Mall, R., Warle, Marien, R., Warle, M., Warle, M
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                         334 CTGCTGCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGG 393
                                                                                                                     394 CAGCGGTACAGCCACGCGGCAGGAGTGTGCTCGCAACGCCACCTGCACCACTACACG 453
                                                                                                                                                                                                                                                  454 CAGCT-CGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCACCTGTGCTCTGCAGG 512
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of a contigs. The true order of the pieces

* consists of a contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                        Center project name: 2UAR
Center clone name: RP43-119N13
Center clone name: RP43-119N13
Sequencing vector: Plasmid; M77789
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.9903309
Consensus quality: 191814 bases at least 040
Consensus quality: 194113 bases at least 030
Consensus quality: 194113 bases at least 020
Consensus quality: 194113 bases at least 030
Consensus quality: 194114 bases 030
Consensus qual
                                   Submitted (13-0cm-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 23, 2001 this Sequence version replaced gi:16258969.

Center: Baylor College of Medicine
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172531: contig of 50625 bp in length
172631: gap of unknown length
180970: contig of 8339 bp in length
181070: gap of unknown length
191108: contig of 10038 bp in length
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                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/db_xref="taxon:9598"
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Direct Submission.

Submitted (02-Nov-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Nov 2, 2001 this sequence version replaced 91:14589452.

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program estimates computed by the Phrap assembly program All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 179675)
DOE Joint Genome Institute.
     PRI 02-NOV-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179675)
DOE Joint Genome Institute.
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INDEPT. 1106 PRI 02-NOV-1 Homo sapiens chromosome 16 clone RP11-419C5, complete sequence. AC026468
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All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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DOE Joint Genome Institute.
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                                                                                              AC026468.6 GI:16596532
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Best Local Similarity
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       Unpublished
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Qy
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 190595)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (07-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA
Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
lerve in 10,000 bp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
Db 46441 CTGCTACCGGGGGTTGGTGTCCTTTGTCGAAGTGGTCAGCCTATGGTTTGCAGAGGGG 46382
                                                                                         ACUU9022 190595 bp DNA linear PRI 07-FEB-2
Phono sapiens chromosome 16 clone RP11-106J23, complete sequence.
ACU09022
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
                                                                  394 CAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCACTGCACCACTACACG 453
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Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN-1 file.
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Pred. No. 3e-38;
0; Mismatches 8; Indels 0;
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/Clone="RPULL_106J23"
91050. .91410
/note="unresolved tandem repeat"
a 43243 c 43697 g 52220 t
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DOE Joint Genome Institute.
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QY 214 CTGGACTGGAGTGACCTGGCCCAACTGGCTCAAGCCAGGCCAGCCCTCTGTGGAATC 273
Db 188925 CAGGACTGGAGTGACAGCCTGGCCCAGGCCAGGCCAGCCCTCTGTGGAACC 188866
                                                                                                                                                                                                                                                  Db 188805 CIGCTACCCGCGGGCTTCGTGTCCTTTGTCGAAGTGGTCAGCCTATGCTTTGCAGAGGG 188746
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                                                                                                                                                                                                                   334 CIGCIGCCCGGGGCTIGGCGICCTTIGIIGAAGIGGICAGCCIAIGGIIIGCAGAGGGG 393
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(without alignments) 7656.298 Million cell updates/sec December 28, 2002, 20:22:13; Search time 99.5384 Seconds GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd. Total number of hits satisfying chosen parameters: 363474 seqs, 203117208 residues OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-09-944-896-49 1876 Title: Perfect score: Scoring table: Sequence: Searched: Run on:

Database :

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

	Description	Care 04 condition	Sociondo 49, Appl.	Sequence 49, Appr	Sequence 40, Appl	Sequence 40 Appl	٠.	Sequence 49, appl	Sequence 10 April	_	n c	•	Sequence 49, Appl			49		,		Sequence IZ, Appl		Sequence 3, Appli	
	ID	US-09-944-413-49	US-09-644-403-49	US-09-944-896-49	US-09-944-49	US-09-866-028-49	US-09-944-449-49	US-09-944-457-49	US-09-945-587-49	US-09-945-015-49	07-90-07-511	000 110 00 01	08-08-844-097-49	US-09-944-432-49	US-09-943-762-49				C C C V J - 3C C - 5U - 5H	03-03-120-043-12	US-09-790-264-1	US-09-790-264-3	
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Sequence 321, App Sequence 872, App Sequence 873, App Sequence 53, Appl Sequence 54, Appl Sequence 55, Appl Sequence 54, Appl Sequence 55,	53, 53, 1, A 15, 75, 222, 1076
US-09-884-411-321 US-09-834-975-872 US-09-834-975-884 US-09-944-413-53 US-09-944-403-53 US-09-944-403-53 US-09-944-403-53 US-09-944-49-53 US-09-944-49-53 US-09-944-487-53 US-09-944-487-53 US-09-944-487-53 US-09-944-07-53 US-09-944-07-53 US-09-944-07-53 US-09-944-07-53 US-09-944-07-53 US-09-944-097-53	4 3 3 3 3 3 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6
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ALIGNMENTS

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APPLICANT: Wood, William TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILLE REPERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/94,413
CURRENT PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: December 1, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
                  Sequence 49, Application US/09944113
Patent No. US20020156004A1
                                                                                                                                                                                                                                                                                                              Grimaldi, Christopher
                                                                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
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Hillan, Kenneth
Kijavin, Ivar
Napier, Mary
Roy, Margaret
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APPLICANT: Botstein, David
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                                                                                                                                                         Eaton, Dan
                                                                        GENERAL INFORMATION:
US-09-944-413-49
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PRIOR PELICATION NUMBER: 60/069,702
PRIOR FILIKO DATE: December 17, 1997
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PRIOR FILIKO DATE: PEDVINATY 5, 1998
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PRIOR PILIKO DATE: PEDCEMBER 16, 1998
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PRIOR APPLICATION NUMBER: 60/113, 206
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Matches 1876; Conservative
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CORGANISM: Homo Sapien
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LENGTH: 1876
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APPLICANT: Botstein, David
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DR APPLICATION NUMBER: PCT/US00/20710

DR FILING DATE: July 28, 2000

DR APPLICATION NUMBER: PCT/US00/32678

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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: P25.48PIC1
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
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APPLICATION NUMBER: PCT/US98/19330
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PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 1001-05-334
PRIOR PELING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR PELING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PELLING DATE: December 16, 1997
                                                                                                                                                                                                Sequence 49, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
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APPLICATION NUMBER: 60/074,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: September 16, 1998
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APPLICATION NUMBER: 60/070,440
ELING DATE: January 5, 1907
APPLICATION NUMBER: 60/074,086
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APPLICATION UNDBER: 60/075, 945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
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APPLICATION NUMBER: 60/113,296
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
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Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
Goddard, Audrey
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US-09-944-896-49
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                                                                                                                           FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020168715Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020168715Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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100.0%; Pred. No. 0;
tive 0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PLEING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR PILICATION NUMBER: PCT/US00/2010
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
LENGTH: 1876
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/224,311
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. US20020168715Alember PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: FEBRUARY 11, 2000
                                                                                                                                                                                                                                                                                                                                                                                               PRILING DATE: February 22, 2000

R APPLICATION NUMBER: PCT/USO0/05841

PR FILING DATE: March 2, 2000

PR APPLICATION NUMBER: PCT/USO0/08439

PR FILING DATE: March 30, 2000

PR APPLICATION NUMBER: PCT/USO0/14042

PR FILING DATE: May 22, 2000

PR APPLICATION NUMBER: PCT/USO0/20710
                                                                                                                                                                                                                                                                FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
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US-09-944-896-49
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781	ATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG 840
841	GACGICICAACAICAGCÁCCIGCCACIGCCACIGICCCCIGGCIACACGGCAGAIACI 900
901	GCCAAGTGAGGTGCAGCCTGCAGTGTGCACGCCCGGTTCCGGGAGGAGTGCTCGT 960
961 961	GCGTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTCCCTTCC 1020
1021	ACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCT 1080
1081	ATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCC 1140
1141	AGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGA 1200
1201	CTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGAGACGGCCAAGG 1260
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1321	1 CTGACAACCAGGGGTGTGTGGCTGAGTGCTGCGGTTTGGCAACTGCGTGGAGC 1380
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APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
PRIOR PAPLICATION NUMBER: US/067,411
PRIOR APPLICATION NUMBER: US/067,411
PRIOR APPLICATION NUMBER: US/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
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Sequence 49, Application US/09944944
Sequence 49, Application US/09944944
Sequence 40. US20020173463A1
GENERAL INFORMATION:
GENERAL INFORMATION:
BAPLICANT: Bacton, Dan
APPLICANT: Faton, Dan
APPLICANT: Faton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Geodard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Grimaldi, Christopher
APPLICANT: Grimaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
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APPLICANT: Napier, Mary
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US200021/3463Alember 30,
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US200201/3463Alember 30,
APPLICATION NUMBER: PCT/US99/2831
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100.0%; Pred. No. 0;
ive 0; Mismatches
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR PELICATION NUMBER: 60/070,440
PRIOR PELICATION NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/074,098
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR PELING DATE: FEBRUARY 9, 1998
PRIOR PELING DATE: FEBRUARY 9, 1998
PRIOR PELING DATE: FEBRUARY 9, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1999
PRIOR PELING DATE: NOW UNBER: PCT/US99/28301
PRIOR PELING DATE: DECEMBER: DCT/US99/28301
PRIOR PELING DATE: SEPTEMBER: PCT/US99/28301
PRIOR PELING DATE: PEDECATION NUMBER: PCT/US99/30095
PRIOR PELING DATE: PEDECATION NUMBER: PCT/US99/30095
PRIOR PELING DATE: PEDECATION NUMBER: PCT/US90/04414
PRIOR PILING DATE: PEDECATION NUMBER: PCT/US90/06841
PRIOR PILING DATE: PEDECATION NUMBER: PCT/US90/06841
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PRIOR PELING DATE: PEDECATION NUMBER: PCT/US90/06
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Matches 1876; Conservative
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APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Ferrara, Napoleone
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APPLICANT: Filvaroff, Ellen
APPLICANT: Godaxaf, Audren
APPLICANT: Godimaldi, Christopher
APPLICANT: Guimaldi, Christopher
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APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
APPLICANT: Nood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLCI
CURRENT APPLICATION NUMBER: US/09/866,028
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Patent No. US20020058309A1
GENERAL INFORMATION:
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iive 0; Mismatches
CURRENT FILING DATE: 2001-05-25 Prior application data removed - NUMBER OF SEQ ID NOS: 120
                                                                                          Conservative
                                                 ORGANISM: Homo Sapien
                                                                         Query Match
Best Local Similarity
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                                  LENGTH: 1876
                                                         US-09-866-028-49
                          SEQ ID NO 49
                                         TYPE: DNA
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Grimaldi, Christopher

Gurney, Austin Hillan, Kenneth Kljavin, Ivar

Ferrara, Napoleone Filvaroff, Ellen

Gerritsen, Mary Goddard, Audrey Godowski, Paul

APPLICANT: APPLICANT: APPLICANT:

APPLICANT

APPLICANT:

Baker, Kevin Botstein, David

Eaton, Dan

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US-09-944-449-49; Sequence 49, Application US/09944449; Patent No. US20020102647A1

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME CHIEF SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME CHIEF SECRETED AND SECRETED A
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Roy, Margaret
Tumas, Daniel
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                                                                                              DR FILING DATE: WO. US.COLOLOLOSO4/ALEMDER)

PRINCIATION NUMBER: PCT/US99/28301

PRELING DATE: December1, 1999

RAPPLICATION NUMBER: PCT/US99/30095

DR APPLICATION NUMBER: PCT/US00/03565

R FILING DATE: February 11, 2000

R APPLICATION NUMBER: PCT/US00/04414

DR FILING DATE: February 22, 2000

R APPLICATION NUMBER: PCT/US00/06419

R PILING DATE: March 2, 2000

DR APPLICATION NUMBER: PCT/US00/08439

R FILING DATE: March 30, 2000

DR APPLICATION NUMBER: PCT/US00/08439

R FILING DATE: March 30, 2000

DR APPLICATION NUMBER: PCT/US00/14042

DR FILING DATE: May 22, 2000

DR APPLICATION NUMBER: PCT/US00/1000

DR APPLICATION NUMBER: PCT/US00/1000

DR APPLICATION NUMBER: PCT/US00/20710

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PRIOR FILING DATE: February 28, 2001
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CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR PRILOWIND NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: DECEMBER 3, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
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PRIOR PILING DATE: DECEMBER 12, 1997
PRIOR PILING DATE: DECEMBER 16, 1997
PRIOR PILING DATE: DECEMBER 17, 1997
PRIOR PILING DATE: DECEMBER 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
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Grimaldi, Christopher
Gurney, Austin
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APPLICANT: Botstein, David
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Roy, Margaret
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020110859Alember 30, 1999
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FILING DATE: No. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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tive 0; Mismatches
PRIOR AFFLICATION NUMBER: 60/075, 945
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 25, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELLING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PELLING DATE: December 16, 1998
PRIOR PELLING DATE: December 16, 1998
PRIOR PELLORATION NUMBER: PCT/US98/19330
PRIOR PELLING DATE: December 16, 1998
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PRIOR PELLING DATE: December 17, 1998
PRIOR PELLING DATE: December 16, 1998
PRIOR PELLING DATE: December 17, 1998
PRIOR PELLING DATE: December 17, 1999
PRIOR PELLING DATE: December 17, 1999
PRIOR PELLING DATE: SEPTEMBER: PCT/US99/12552
PRIOR PELLING DATE: SEPTEMBER: PCT/US99/21090
PRIOR FILING DATE: SEPTEMBER: PCT/US99/21090
PRIOR FILING DATE: SEPTEMBER: PCT/US99/21090
PRIOR FILING DATE: NO. USSOURCHIBER
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PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: JUJY 28, 2000
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PRIOR APPLICATION NUMBER: PCT/US00/32678
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
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PRIOR APPLICATION NUMBER: PCT/US00/04414
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Best Local Similarity 100.
Matches 1876; Conservative
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; ORGANISM: Homo Sapien
US-09-944-457-49
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Qy Db	241	CCGGAGCCCTGAACAGGAAGAGTTTCTTGCTCCTCTCCT	0
Qy	301	GCTGGGTCCAGCCCCTGCGGCTGACATGCGGAGGTGGACTGGAGTGACAGCCTGGGCC 36	360
o do		ACTGGCCCAAGCCAGGGCACCCTCTGGAATCCCAACCCGAGCTGGCATCCGGCC 4 ACTGGCTCAAGCCAGGCACCCTCTGTGAATCCCAACCCGAGCTGGCATCCGGCC 4 ACTGGCTCAAGCCAGGCAGCCTTGTGGAATCCCAACCCGGAGCTGGCATCCGGCC 4 ACTGGCTCAAGCCAAGCCCAGCCCTCTGTGGAATCCCCAACCCGGGCTTCGGCATCCGGCC	0 0
Qy Db	421	TGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGCGGGGTTGGCGTCCT 4	
Qy Db	481	GGTCAGCCTATGGTTTGCAGAGGGCAGCGGTACAGCCACGCGGCAGG 	
Qy Dp	541	TGTGCTCGCAACGCCACCTGCACCACTACACGCAGCTCGTGTGGGCCACCTCAAGCC	
Qy	601	ATAGAAGCCTTTGTCT 6	099
Qy Dp	661	ATCCCCTATAAGA 7	Ø Ø
Qy	721	AAAGCCTGGGACC 7:	<u>ω</u> ω
Qy	781	GAATCCTTGTCGCATGAGCTGCCAGAACCATG 8 11 1 1 1 1 1 1 1 1	140
Oy Db	841	CAGCACCTGCCACTGCCCCCTGGCTACACGGGCAGATACT 9	0 0
Qy	901	SIGAGGIGCAGCCIGCAGIGIGGACGGCCGGIICCGGGAGGAGGAGGAGGCIGCICGI 9	9 9
Qy Dp	961	CCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC 1	02
oy Db	1021	GGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCT 1	080
Oy Ob	1081	CAGAGCCAGGATGAAATGTCAGAGGAAGGCGGGGTGCTGGCCCAGATCAAGAGCC 1.	140
ςς Ωp	1141	AAAGTGCAGGACATCCTGGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGA 1	
λ G G		*IGACTICGAGACCAGGAACTICTGGATCGGCTCACCTACAAGACCGCCAAGG	260
QQ AQ	1261	ICCTICCGCTGGGCCACAGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGC 1	320

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1321 CTGACAACCACGGGCTGGTGTGGCTGAGTGCCATGGGGTTTGGCAACTGCGTGGGAGC 1380
                                                                     CTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGC 1380
                                                     TGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACA 1440
                                                                                                           TCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCA 1500
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                                                                                                                           FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR PAPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Napier, Mary
Roy, Margaret
Tumas, Daniel
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PRIOR FILING DATE: December 11, 1997
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PRIOR APPLICATION WINBER: 60/069 870
PRIOR APPLICATION WINBER: 60/0769 870
PRIOR PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION WINBER: 60/076 980
PRIOR PRIOR PRIOR FEBRUARY 9, 1998
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      24.1
      CCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCCTGCACACCGCCTGCGCA

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Pred. No. 0;
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                                                           Best Local Similarity 100.
Matches 1876; Conservative
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo Sapien
                     ; ORGANISM: HOI
US-09-945-587-49
                                                    Query Match
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Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Ferrara, Napoleone
                       Gerritsen, Mary
Goddard, Audrey
                                                                                      Hillan, Kenneth
                                                                                                   Kljavin, Ivar
                                                                                                               Napier, Mary
Roy, Margaret
                                                                                                                                                    Wood, William
                                                                                                                                         Tumas,Daniel
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Sequence 49, Application US/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baten, David
APPLICANT: Eaton, Dan
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TELE REPERBRES: P2548PILL CURRENT APPLICATION NUMBER: US/09/945,015 CURRENT FILING DATE: 2001-09-26
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PRIOR FILING DATE: NO. US20020132768Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-26
PRIOR FILING DATE: 2001-05-26
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1998
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PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: PEDIUARY 9, 1998
PRIOR FILING DATE: FEDIUARY 9, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: DECEMBER: 09/254, 311
PRIOR PRILICATION NUMBER: 09/214, 311
PRIOR PRILICATION NUMBER: 09/254, 311
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PRIOR FILING DATE: September 15, 1999
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PRIOR APLICATION NUMBER: PCT/US00/03565
PRIOR APPLICATION NUMBER: PCT/US00/03656
PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR PLING DATE: March 2, 2000
PRIOR PLING DATE: March 3, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: May 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: PEDCOMINGO/32678
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Best Local Similarity 100.
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781 ATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG
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                                 GTGCCTACTCCCCCGGGGGGGGAGCTCAACGGGGAAGACAATCATCCCCTATAAGA
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                    1741 GAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCC
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CURRENT APPLICATION NUMBER: US/09/944,396

CURRENT APPLICATION NUMBER: US/09/944,396

CURRENT APPLICATION NUMBER: US/09/944,396

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR PILING DATE: DOCEMBER 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR APPLICATION NUMBER: 60/069,337

PRIOR APPLICATION NUMBER: 60/069,378

PRIOR PILING DATE: DECEMBER 11, 1997

PRIOR PILING DATE: DECEMBER 16, 1997

PRIOR PILING DATE: DECEMBER 17, 1997

PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR PILING DATE: DECEMBER 17, 1997

PRIOR APPLICATION NUMBER: 60/069, 017

PRIOR APPLICATION NUMBER: 60/069, 017

PRIOR APPLICATION NUMBER: 60/069, 017

PRIOR APPLICATION NUMBER: 60/0704, 440

PRIOR FILING DATE: DECEMBER 18, 1997

PRIOR APPLICATION NUMBER: 60/0704, 099

PRIOR FILING DATE: DECEMBER 18, 1997

PRIOR APPLICATION NUMBER: 60/0704, 099

PRIOR PILING DATE: EPENUARY 5, 1998

PRIOR PILING DATE: FEBRUARY 9, 1998

PRIOR PILING DATE: FEBRUARY 9, 1998

PRIOR PILING DATE: FEBRUARY 9, 1998
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FILING DATE: February 9, 1998
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Patent No. US20020132981A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Roy, Margaret
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US-09-944-396-49
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FILING DATE: NO. US2020012281Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020132981Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
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DR APPLICATION NUMBER: 09/218,517
DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 09/254,311
DR FILING DATE: March 3, 1999
DR FILING DATE: June 22, 1999
DR APPLICATION NUMBER: PCT/US99/21090
DR APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
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APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
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FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US00/20710
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US00/03565
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APPLICATION NUMBER: PCT/USO0/32678
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                                                                                                                                                                                              APPLICATION NUMBER: PCT/US98/19330
                                                                                                                                                                                                                         FILING DATE: September 16, 1998
APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
FILING TOATE: December 20,113,296
FILING DATE: December 22, 1998
                                                                                                                           APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
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                                                        PRIOR APPLICATION NUMBER: 6
PRIOR FILLING DATE: December
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PRIOR PILLING DATE: SEPTEMBER: P
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CCGGAGCCCTGAACAGGAAGAGAGTTTCTTGCTCCTCTCCCTGCACAACGCCTGCGCA	GCTGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCC	AACTGGCTCAAGCCAGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCCCAALLIIIIIIIIIIIIIIIIIIIIIIIIIIII	TGTGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGCGGGGCTTGGCGTCCT	TTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGGAGCGGTACAGCCACGCGGCAGGGG 	AGTGTGCTCGCAACGCCACTGCACCACTACACGCAGCTCGTGTGGGCCACCTCAAGCC 	AGCTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCT 	. GTGCCTACTCCCCCGGAGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGA	. AGGGTGCCTGGTGTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGACCCTGGACCCTGGACCTGCTGCTGCTGCTGGACCTGGACCTGGGCTGCTTGTTTTTTTT	. ATGCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG	GACGTCTCAACATCAGCACTGCCACTGCCACTGTCCCCTGGCTACAGGGGCAGATACT	GCCAAGTGAGGTGCAGCCTGCAGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGT	GCGTCTGTGACATCGGCTACGGGGGGGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC	. ACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCT	. ATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCC 	. AGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGA 	. CTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGG	ACTCCTTCGGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTGCCTTTGGGCAGC	CTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGC
241	301	361	421	481	541	601	661	721	781	841	901	961	1021	1081	1141	1201	1261	1321
qq	Qy Db	Qy Db	QY Db	QY	QY	QY Db	Qy Db	Qy Db	Qy Db	QY	Qy Db	Oy Dp	Qy Db	QY Db	Qy	Qy	QY	QY

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APPLICANT: NOW, MARTGATE, TARGED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ATTLLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/944,097

CURRENT FILING DATE: 2001-08-31

PRIOR FILING DATE: 2001-08-35

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: DECEMBER: 60/069, 238
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                TCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCA
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Gurney, Austin
Hillan, Kenneth
Kijavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
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Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
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APPLICANT: Botstein, David
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Godowski, Paul
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US-09-944-097-49
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020138675Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020133675Alember 30, 1999
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PRILOR TOWN NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: Pebruary 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR APPLICATION NUMBER: 60/105, 945
PRIOR PELING DATE: Pebruary 9, 1998
PRIOR PELING DATE: Pebruary 9, 1998
PRIOR APPLICATION NUMBER: 60/116, 1298
PRIOR PELING DATE: SEPTEMBER 16, 1998
PRIOR PELING DATE: SEPTEMBER 16, 1999
PRIOR PELING DATE: SEPTEMBER: PCT/USS9/289131
PRIOR PELING DATE: SEPTEMBER: PCT/USS9/289131
PRIOR PELING DATE: SEPTEMBER: PCT/USS9/289131
PRIOR PELING DATE: DECEMBER: PCT/USS9/289131
PRIOR PELING DATE: DECEMBER: PCT/USS9/289131
PRIOR PELING DATE: PEDTUARY 22, 2000
PRIOR APPLICATION NUMBER: PCT/USS9/289/199
PRIOR PELING DATE: MATCH 2, 2000
PRIOR APPLICATION NUMBER: PCT/USS9/28919
PRIOR PELING DATE: MATCH 2, 2000
PRIOR PELING DATE: MATCH 2, 2000
PRIOR APPLICATION NUMBER: PCT/USS9/28919
PRIOR PELING DATE: MATCH 2, 2000
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PRIOR PELING DATE: JULY 28, 2000
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ORGANISM: Homo Sapien
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LENGTH: 1876
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FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
FPLING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
Gurney, Austin
Hillan, Kenneth
                            Kljavin, Ivar
                                                        Roy,Margaret
                                                                   Tumas, Daniel
                                         Napier, Mary
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                                                                                               1141 AGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGCCACCAACGAGGTGA 1200
                            ATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCC 1140
                                                                                1141 AGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGA 1200
1021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCT 1080
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Patent No. US20020142419A1
GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Ferrara, Napoleone
Filvaroff, Ellen
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APPLICANT: Botstein, David
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APPLICANT: Thursts, Daileled
APPLICANT: Wood, Millian
APPLICANT: Wood, Millian
APPLICANT: WOOD, Millian
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CURRENT FILM OF APPLICATION WHARE: 05/09/244/432
CURRENT FILMS DAFE: 2001-09-26
PRIOR FILMS DAFE: 2001-09-26
PRIOR FILMS DAFE: 2001-09-26
PRIOR FILMS DAFE: December 11, 1997
PRIOR FILMS DAFE: December 11, 1997
PRIOR PLILNS DAFE: December 11, 1997
PRIOR PLILNS DAFE: December 11, 1997
PRIOR PLILNS DAFE: December 11, 1997
PRIOR PAPLICATION WHARE: 60/06/335
PRIOR PAPLICATION WHARE: 60/06/335
PRIOR PAPLICATION WHARE: 60/06/34
PRIOR PAPLICATION WHARE: 60/06/36
PRIOR PAPLICATION WHERE: 60/06/36
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PRIOR PELLING DATE: March 3, 2000
PRIOR PELLING DATE: March 30, 2000
PRIOR PELLING DATE: May 22, 2000
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PRIOR PILING DATE: JUJY 28, 2000
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PRIOR PELLING DATE: DECEMBER: PCT/US00/20710
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PRIOR APPLICATION NUMBER: PCT/US01/06520
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NUMBER OF SEQ ID NOS: 120
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                      1801 TGTGGGGCAGCGGAGCTTCCCTGTGGGCATGAACCCCACGGGGTATTAAATTATGAATCAG 1860
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APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILLING DATE: 2001-05-25
PRIOR PILLING DATE: 2001-05-25
PRIOR PLILING DATE: 2001-05-25
PRIOR PLILING DATE: December 3, 1997
PRIOR FILLING DATE: December 11, 1997
PRIOR FILLING DATE: December 12, 1997
PRIOR FILLING DATE: December 12, 1997
PRIOR FILLING DATE: December 12, 1997
PRIOR FILLING DATE: December 16, 1997
PRIOR FILLING DATE: December 17, 1997
PRIOR FILLING DATE: PEDVILOXING, 440
PRIOR FILLING DATE: FEDVILOXING, 9, 1998
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PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
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                                                                                                                                                                                                                                                                                            Sequence 49, Application US/09943762
Patent No. US20020142958A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff,Ellen
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Hillan, Kenneth
Kljavin, Ivar
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APPLICANT: Botstein, David
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PRIOR FILING DATE: December 21, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3 1999
PRIOR FILING DATE: March 3 1999
PRIOR FILING DATE: March 3 1999
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: SEPTEMBER: PCT/US99/21090
PRIOR FILING DATE: SEPTEMBER: PCT/US99/28409
PRIOR PRILING DATE: NO. US20020142958Alember 30, 1999
PRIOR FILING DATE: NO. US20020142958Alember 30, 1999
PRIOR FILING DATE: NO. US20020142958Alember 30, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: FEDULARY 21, 2000
PRIOR FILING DATE: FEDULARY 21, 2000
PRIOR FILING DATE: FEDULARY 21, 2000
PRIOR PELING DATE: FEDULARY 21, 2000
PRIOR PELING DATE: FEDULARY 31, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR PELING DATE: MARCH 30, 2000
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PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR PELING DATE: DECEMBER: PCT/US00/2678
PRIOR PELING DATE: MARCH 30, 2000
PRIOR PELING DATE: PEDULARY 28, 2001
PRIOR PELING DATE: PEDULARY 28, 2001
PRIOR PELING DATE: FEDULARY 28, 2001
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PRIOR PELING DATE: FEDULARY 28, 2001
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100.0%; Pred. No. 0;
tive 0; Mismatches
                               FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
PRIOR APPLICATION NUMBER: PCT/US98/19330
                                                                              PRIOR APPLICATION NOTICE 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION UNMBER: 09/216,021
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ORGANISM: Homo Sapien
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Best Local Similarity
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1681 AGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740
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APPLICANT: Tunas, Dailel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
                                                              1501 CATGGCTCCCTCGCCTGGCACCGGCTCTGCTTACCTGTCTGCCACCTGTCT
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/66/028
PRIOR APPLICATION NUMBER: 60/66/411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/669/334
PRIOR FILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
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PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
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FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
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Patent No. US20020142959A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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Napier, Mary
Roy, Margaret
Tumas, Daniel
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Roy, Margaret

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1081 ATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCC 1140
                            1201 CTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGG 1260
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                                                                                     1261 CTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGG
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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Hillan, Kenneth
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US-09-943-851A-49
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020150976Alember 30, 1999
                                                                                                                          FILE REFERENCE: P2548PL01
CURRENT APPLICATION NUMBER: US/09/943,851A
CURRENT FILING DATE: 2001-08-30
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BR FILLING DATE: December 16, 1998
BR PELLING DATE: December 22, 1998
BR FILLING DATE: December 22, 1998
BR APPLICATION NUMBER: 09/254,311
BR APPLICATION NUMBER: PCT/US99/12252
BR APPLICATION NUMBER: PCT/US99/12252
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
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PRIOR FILING DATE: December 11, 1997
PRIOR PLING DATE: December 11, 1997
PRIOR PLING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
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PRIOR FILING DATE: DECEMBER: 09/218, 311
PRIOR APPLICATION NUMBER: 07/1059/218, 311
PRIOR APPLICATION NUMBER: 07/1059/218, 311
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PRIOR FILING DATE: 2001-05-25
PRIOR PAPELICATION NUMBER: 60/067,411
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                                Wood, William
       Tumas,Daniel
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PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR PILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/20710
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDTUROL/06520
PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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Search completed: December 28, 2002, 23:04:18 Job time: 104.538 secs

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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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em_gss_pro:* em_gss_rod:*

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	Description	A1792411 an34b09.y BM547887 AGENCOORT BM924615 AGENCOURT B1760121 603044615 B1759120 603042530 B1517774 603042018
SUMMARIES	ID	A1792411 3 BM547887 4 BM924615 3 B1760121 8 B1759120
	Query core Match Length DB II	463 9 1076 13 1034 14 710 13 709 13 928 13
ф	Query Match	99.4 98.1 94.2 93.2
	Score	245.4 242.2 242.2 232.6 230.2
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ALIGNMENTS

		an34b09.y5 Gessler Wilms tumor Homo sapier	INHIBITOR. ;, mRNA Sequence.		AI792411.1 GI:5340127	EST.	human.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Fureleostomi.	Mammalia; Eutheria; Primates; Catarrhini: Hominidae, Homo	1 (bases 1 to 463)		National Cancer Institute / National Institute of Dental Research		Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	This clone is available royalty-free through LLNL ; contact the	IMAGE Consortium (info@image.llnl.gov) for further information	This read is a RESEQUENCE of a previously sequenced himan clone	Original clone citation: see original entry for original citation	information	This 5' resequenced clone has no previous 5' data to verify this	new read against	38q Primer: -40RP from Gibco	nigh quality sequence stop: 429.
RESULT 1 AI792411	LOCUS	DEFINITION	٠	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT										

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241 GGCTGGA 247
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E 1 (bases 1 to 1076)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Oppublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM12735 row: a column: 18
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AGENCOURT_6531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633
                                                                                                                                                           /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; RNA was prepared from a pool of 6 anonymous Wilms' tumor RNAs. RNA was prepared by acid-phenol, followed by one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                      coligo dT selection. CDNA library preparation was with the BRL/Life Tech. Superscript Plasmid system. An oligo-dT NotI primer for first strand synthesis generated geggegecc(t) at the 3' end of the clones. A 5' Sall adaptor was used with sequence 5'-gtcgacccacgcgtccg-3'. Resulting cDNAs were size selected (average size 2 kb). NotI digested, and ligated into NotI/Sall-cut pSPORTI. Library was constructed by Dr. Manfred Gessler."
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                                                                              /clone_lib="Gessler Wilms tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                         /organism="Homo sapiens"
                                                               /db_xref="taxon:9606"
Location/Qualifiers
                                                                                                                          /sex="pooled (6)"
                                                                                                                                              /lab_host="DHi0B"
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BM924615
AGENCOURT_6767842 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5761001
                                                                                                                                                                                                                                                                                          destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
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NIH-MGC http://mgc.nol.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                             /tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 others
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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                                                                                                                                                             /clone="IMAGE:5732633"
/clone_lib="NIH_MGC_124"
                                                                                                      /organism="Homo sapiens"
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High quality sequence start: 9 High quality sequence stop: 677.
                                                                                                                                      /db_xref="taxon:9606
                                                      Location/Qualifiers
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Homo sapiens
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Email: cgapbs-rémail.nih.gov
Email: cgapbs-rémail.nih.gov
Enail: cgapbs-rémail.nih.gov
Enail: cgapbs-rémail.nih.gov
EDNA Library Preparation: Life Technologies, Inc.
EDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                          /clone_lib="NIH_MGC_116"
                                                                                                                               /clone="IMAGE:5761001"
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      Location/Qualifiers
                                                                                                                                                                                         /lab_host="DH10B
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pCMV-SPORT6: Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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pool of 2
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603042530F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182999 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAM11456 row: 1 column: 08
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                                                                                        /clone="IMAGE:5184962"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                        /organism="Homo sapiens"
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Location/Qualifiers
                                                               /db_xref="taxon:9606
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Best Local Similarity 98.3%;
Matches 235; Conservative
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/clone="IMAGE:5182397"

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                                            /note="Organ: pooled colon, kidney, stomach; Vector: pcMv-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 928)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Onpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.go.
Plate: LLAM11455 row: c column: 06
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Tissue Procurement: Life Technologies, Inc.
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/db_xref="taxon:9606"
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Location/Qualifiers
                    /clone_lib-"NIH_MGC_116"
/clone="IMAGE:5182999"
                                      /lab_host="DH10B"
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BI517774
BI517774.1 GI:15342566
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Matches 243; Conservative
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BI517774
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BI757380
603029310F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5199674 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 939)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                       DB 13; Length 928;
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93.2%; Score 230.2; DB 13; Length
Best Local Similarity 98.4%; Pred. No. 4.2e-45;
Matches 243; Conservative 0; Mismatches 3; Indels
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/db_xref="taxon:9606"
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Location/Qualifiers
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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/clone="IMAGE:5199674"

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                               /note="Organ: Drain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EccRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1:5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
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603043573F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183898 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 500)
                                                                                                                                                                                                                                                                                                                                61 GAGAGITICITGCICCICCICCTGCACAACCGCCIGCGAGGIGGGICCAGCCCCTGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
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Clone distribution MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11459 row: a column: 19
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                                                                                                                                                                                                                                                  DB 13; Length 939;
                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                           92.6%; Score 228.6; DB
98.0%; Pred. No. 1e-44;
Live 0; Mismatches
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
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/clone_lib="NIH_MGC_116"
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Location/Qualifiers
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BI761101
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BI761101
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//note="Organ: pooled colon, kidney, stomach; vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code
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603048444F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188643 5',
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
http://image.llnl.gov
Plate: LLAM11471 row: g column: 12
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High quality sequence stop: 849.
Location/Qualifiers
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/clone="IMAGE:5188643"
/lab_host="DH10B"
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BI762690
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/lab_host="DH10B"

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    /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed): RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH.MGC Library."
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603046141F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5186219 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (basea I to 836)
INTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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Clone distribution: MGC clone distribution information can be
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0; Mismatches 2; Indels
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Plate: LLAM11465 row: b column: 12
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Best Local Similarity 98.4%; Pred. No. 1.3
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/db_xref="taxon:9606"
/clone="IMAGE:5186219"
/clone_lib="NIH_MGC_116"
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Location/Qualifiers
/lab_host="DH10B"
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BI764403
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/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MCC Library."
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1 (bases 1 to 916)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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603043013F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5183330 5',
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/lab_host="DH10B"
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/clone="IMAGE:5183330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        916 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BI759353
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                                                                                                                                                                                                                                                                                 157 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                   BASE COUNT
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BI759353
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KEYWORDS
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ò g δ g ò qq δλ g ò qq

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female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MCC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 521)
Frahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, N.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 AGGAGAGTTTCTTGCTCCTCTCCTCCTGCACCCCTGTCGCAGCTGGGTCCAGCCCCCT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                  223 GAGGIGIGGCCACCACCAGCTGCATGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTG-CGCAGCTGGGTCCAGCCCCCT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 GCGG-CTGACATGCGGAGGCTGGACTGGAGTGACA-GCCTGGCCCCAACTGGCTCAAGCCA 175
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                                                                                                                                                                                                                                                                                                                                      5.
                                                                                                                                                                                                                                                                                  Score 190.4; DB 13; Length 916;
Pred. No. 1.3e-35;
0; Mismatches 1; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b1340175 521 bp mRNA linear 365365 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
B1340175
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/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
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Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                  77.18;
97.68;
                                                                                                                                                                                                                                                                               Query Match 77.15
Best Local Similarity 97.65
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AAGTGGGCTGGA 247
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ACCESSION
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BI340175
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COMMENT
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KEYWORDS
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
Fax: 402 762 4390
Fax: anith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PGW SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 188 c 160 g 81 t
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/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
                                                                                                                                                                                                                                                                                                               118 GCGGCTGACAIGCGGAGGCTGGACTGGGTGACAGCCTGGCCCAACTGGCTCAAGCCAGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                      1 GAGGTGTGGCCACCCCAGCTGCAGG---AGCAGGCTCCGATGGCCGGAGCCCTGAACAGG 57
                                                                                                                                                                                                                                                                                                                                                                                                                   178 GCAGCCCTCTGTGGAATCCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAA
                                                                                                                                                                                                   .;
                                                                                                                                                            DB 13; Length 521;
                                                                                                                                                                                                   44; Indels
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77836 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
AW437073
                                                                                                                                                          66.2%; Score 163.6; DB 1:81.2%; Pred. No. 3.1e-29; iive 0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .392
/organism="Sus scrofa"
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Plate: 37 row: H column: 9
Seq primer: ATTTAGGTGACACTATAG.
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PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW437073.1 GI:6972379
                                                                                                                                                                           Best_Local Similarity 81.23
Matches 203; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 GTGGGCTGGA 247
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Sus scrofa
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                                                                                                                                                            Query Match
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                                                                                                 BASE COUNT
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34; Indels

Mismatches

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Matches 180; Conservative
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                                                                                                                                                                                                                                                                                                                                                       RESULT 15
AW786132
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VERSION
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Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine (Unpublished (2000))
Contact: Smith TPL
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 321)
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                                                                                                                                                                                                          CTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGG 135
                                                                                                                                                                                                                                                               213 CTCTCGCTGCCACAACCGCCTGCGCAGCCGGCTCCCCCCTGCAGCCAACTGCAGAA 272
                                                                                                                                                                                                                                                                                                                     136 CTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATC 195
                                                                                                                                                                                                                                                                                                                                        273 ATGGACTGGAGTGAGAGGCTGGCTCAACAGGCTCAGACCAGGGCGGCCCTTTGTGTGGCGCC 332
Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 136 c 124\ g 63\ t
                                                                                                                                 0; Gaps
                                                                                                                                                                    Score 135.6; DB 13; Length 321; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                              196 CCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTGCAAGTGGGCTGGA 247
                                                                                                                                                                                                                                                                                                                                                                                                                 333 CCAGCCCCAAGCCTGGCTTCCATCCTCCGGGCTGCACCCCAAGTGGGCTGGA 384
                                                                               Score 162; DB 10; Length 392;
Pred. No. 7.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384181 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI359591
                                                                                                                           0; Mismatches 44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 bp
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/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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82.6%;
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Best Local Similarity 81.0%;
Matches 188; Conservative
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Single pass sequencing. Bases called and alt_trimmed with phred v0.880904.v. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20,
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                                                                                                                                                                                                                                164 AAGGAGAGCTTCTTGCTCCTCTCGCTGCACAACCGCCTGCGCAGCCGGGTCCACCCCCCT 223
                                                                                                                                                                                                   118 GCGGCTGACATGC-GGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAG 176
                                                 104 GAAGIGCAGCCACTTCAGCTGCAGGAGAAGCAGGTTCCAATGCCCGGAGCCCTGAGCAGG 163
                                                                                                   AAGGAGAGTITCITGCTCCTCCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCT 117
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1 GAGGTGTGGCCACCCCAGCTGCAGG---AGCAGGCTCCGATGGCCGGAGCCCTGAACAGG 57
                            Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118625 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. AW786132
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                         177 GGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCAT 214
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84.1%; Pred. No. o...
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/db_xref="taxon:9823"
/clone_lib="MARC lpIG"
/tissue_type="pooled"
/lab_host="DH10B"
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- Db Qy
 - - qq
- 178 GC 179 || 522 GC 523 δy

Search completed: December 28, 2002, 20:45:42 Job time : 333.93 secs

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December 28, 2002, 16:45:43; Search time 2505.87 Seconds (without alignments) 12124.644 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query				
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1	861.6	45.9	1034	14	BM924615	BM924615 AGENCOURT
2	790.6			13	BM547887	TANAL TARA TARA
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					#///TCTG	8T07*0\$00 *///TCTS
7	754			13	BI764403	BI764403 603046141
2	9.629			13	BI757380	BI757380 603029310
9	929			13	BI760121	BI760121 603044615

BI759120 603042530 BM695392 UI-E-CQ1- BI779535 603043013 BT750500 60304044	14	ກແ	BQ006636 UI-H-EII-	AW299257 xs48f01.x	JI-H-EU	BQ720124 AGENCOURT	AI989724 ws35h02.x	AI433291 ti86b01.x	AW001740 ws04c06.x	AI627475 ty80a06.x	AW451907 ŪI-H-BI3-	AA976491 oq71e08.s	AI792411 an34b09.v	BG150347 7199a09.x	AI150446 qf41a03.x	AI589178 tn48a03.x	BI761101 603043573	AI827695 wf11a11.x	BE552150 hw29q03.x	BM708158 UI-E-CII-	AW137750 UI-H-BI1-	AI863534 wh72f06.x	AA903561 ok63a05.s	BF527554 602040477	AA812725 aj31h02.s	BF198258 248012 MA	AI657201 tt50d10.x	365365	d72d09.r	AA582202 nn48f01.r	BG608968 322458 MA	EST3849	60304560	AI942280 wo79a05.x
BI759120 BM695392 BI759353	AI307814	ALU40183 BF057185	BQ006636	AW299257	BQ446805	BQ720124	AI989724	AI433291	AW001740	AI627475	AW451907	AA976491	AI792411	BG150347	AI150446	AI589178	BI761101	AI827695	BE552150	BM708158	AW137750	AI863534	AA903561	BF527554	AA812725	BF198258	AI657201	BI340175	W79362	AA582202	BG608968	AW972808	175973	AI942280
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636.6 622.2 610.2 589	580	568.6	564.4	564	556.4	513.8	490.2	487.6	487.4	487	453.4	448.4	444.8	443.8	439	432	419.8	410.8	402.6	401.8	376.2	352.2	339	328	325.2	313.4	304	299.2	297.2	286.4	271.6	265	257	241
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ALIGNMENTS

BM924615 AGENCOURT_6767842 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761001 5', mRNA sequence. BM924615 BM924615.1 GI:19374994 EST. human.	Lukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1034) 1NH MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Email: cgapbs.rémail.nih.gov Tissus Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	Figure: LLAWIZBUB row: o column: 18 High quality sequence stop: 685. Location/Qualifiers 11034
RESULT 1 BM924615 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES Source

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                                                            /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                        56; Indels
                                                                                                                                                                                                                                                                        Score 861.6; DB 14;
Pred. No. 1.2e-183;
0; Mismatches 56;
                      /clone="IMAGE:5761001"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                        vuery Match 45.9%;
Best Local Similarity 93.6%;
Matches 953; Conservative
                                                                                                                                                                                                             023. NC.
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AGENCOURT_6531767 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732633 BM547887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
721 GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCANAGCCTGGGACCAT 780
                                           841
                                                              781 GCAGGGGGGCCTCTGTGAGGTCCCCAAGGATCCTTGTCGCATGAGCTGCCA-AAACATGG 839
                                                                                                                                                        CCAAGTGAGGTGCAG-CCTGCAGTGTGTGCACGGCCGGTTCCGGG-----AGGAGGAGTG 955
                                                                                                                                                                                                                                               ACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTG 901
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                                              GCA - GGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGG
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)
                                                                                                                                                                                                                                                                                                                                   960 TIGCCTCCTTTAACATCGGCTAGGGGGGAACCCAGGGTGCCCCCAGGGGGCATTT
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High quality sequence stop: 677.
Location/Qualifiers

1. 1076
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5732633"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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BI517774 928 bp mRNA linear EST 29-AUG-2001 603042018F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5182397 5',
                                             188
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                                                      189 ACCACCTGGGCAGGGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
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BI517774
BI517774.1 GI:15342566
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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/note="Organ: pooled colon, kidney, stomach; Vector: pcMV-SPORT6: Site_1: Not1: Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1: 4 kb, insert size range 1:3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NTH_MGC Library."
                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM1455 row: c column: 06
High quality sequence stop: 860.
                 1 (bases 1 to 928)
NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                     1. 928
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182397"
/clone_llb="NHL WGC_116"
/lab_host="DH10B"
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                                                       TITLE
JOURNAL
COMMENT
               REFERENCE
AUTHORS
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Score 754; DB 13;
Pred. No. 2e-159;
                                                                                                                              Ouery Match 40.2%; Score 754; DB Best Local Similarity 97.7%; Pred. No. 2e-1 Matches 807; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: ggapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1465 row: b column: 12
High quality sequence stop: 761.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) (Uppublished (1999)
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                                                                                                                                                                                                                                     660 GGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCA 719
                                                                                                                                                                                                                                                                                                       720 TGCAGGGGGGCTCCTGTGAGGTCCCCAGGAATCCTTGGTCGCATGAGCTGCCAGAAACCAT 779
542 GTGTGCTCGCAACGCCACCTGCACCTACACGCAGCTCGTGTGGGCCACCTCAAGCCA 601
                                                                                                                                  721
                                                                                                                                                     TGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTT-GTCGCATGAGCTGCCAG-AACCAT
                 480 GTGTGCTCGCAACGCCACCTGCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCA
                                                                                   662 TGCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAA
                                                                                                                                                                                                                                                                                                                                           840 GGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATAC
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/db_xref="taxon:9606"
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destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 02.3. Note: this is a NHLMGC Library."
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                                                                                                                                                                                                                                                                                                  61 GCACAACCGCCTGCGCAGCTGCAGCTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTG 120
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/lab_host="DH10B"
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NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Righ quality sequence stop: 778.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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1. 710

/organism="Homo sapiens"
/db_zer=[largen: 1.0]
/organism="Homo sapiens"
/db_zer=[largen: 1.0]
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/lab_lbost="Holl0"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
n. column: 03
High quality sequence stop: 704.
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494 CAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAA 553
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                     420 CAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGTGTGCTCGCAA
                                                                                                                                           554 CGCCACCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGGCTGTGG
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Contact: Robert Strausberg, Ph.D.
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BI760121
BI760121.1 GI:15751699
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                      Gaps
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                      1;
Length 710;
                      Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Score 676; DB 13;
Pred. No. 7.2e-142;
                     0; Mismatches
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603042530F1 NIH_MGC_116
mRNA sequence.
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BI759120.1 GI:15750698
36.0%;
98.4%;
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http://image.llnl.gov
plate: LLAM11456 row: 1 column: 08
High quality sequence stop: 709.
Location/Qualifiers
i. 709
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/done="IMAGE:5182999"
/clone="IMAGE:5182999"
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/clone="IMAGE:5182999"
/clone="IMAGE:5182999"
/clone="Cryan: pooled colon, kidney, stomach; Vector: pcWv-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 solons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRv site is olise-troyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                                                                                                                                                                                                                                   BM695392 645 bp mRNA linear EST 28-FEB-2002 UI-E-CQ1-aev-n-19-0-UI.rl UI-E-CQ1 Homo sapiens cDNA clone UI.E-CQ1-aev-n-19-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                  601 AGCTGGGCTGTGGGCGCCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match Best Local Similarity 99.5%; Pred. No. 9.4e-130; Matches 624; Conservative 0; Mismatches 3: Tndple 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UT-E-CQ1-aev-n-19-0-UI"
/clone_lib="UT-E-CQ1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
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187 c 19
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linear EST 25-SEP-2001
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603043013F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183330 5',
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11457 row: j column: 03
High quality sequence stop: 723.
Location/Qualifiers
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                                                                                                                         61 CCTGGGACCATGCAGGGGGGCTCTGTGAGATCCCAGGAATCCTTGTCGCAGAGCTGCC 120
                                                                                                                                                                                             891
712 CCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAG 771
                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                               772 CCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCC
                                                                                                                                                                                               832 AGAACCATGGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGG
                                                                                                                                                                                                                                                                                          GCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGGCAGCCTGACAACCACGGGCTGG 1338
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BI759353
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121 CCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCATGCTGCATCCAGAGACCTCCCTGGCCGGGGGCATCTCCTG-GCTGTGCTCCTGGCC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCCCGGACCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCCTGCACACGCCTG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCGGCCTGTGGCGCACCCTGCAAGTGGGCTGGAACA-TGCAGCTGCTGCCCGCGGGGCTT 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 32.5%; Score 610.2; DB 1 al Similarity 91.6%; Pred. No. 5.1e-127 822; Conservative 0; Mismatches 58
1. 916
/organism="Homo sapiens"
                                                                                                       /clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                           /clone="IMAGE:5183330"
                                                  /db_xref="taxon:9606"
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/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 1 yo male colon: 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                               EST 25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 852)
                                                                                                                                                                                                                                                                                                                                                                                                     603048444F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188643 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMINIT row: g column: 12
High quality sequence stop: 849.
Location/Qualifiers
767 CAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAG 826
                                                                                                                                800 C-AAGCCTGTGGACCTGCCGGGGGCCTCTGTGAGGTCCCAGGGAATCCTTGTCCGCATGA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCCAACAGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 AGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGTGCCTGACGGGCCCAACAGAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.4%; Score 589; DB 13; Length 852; 96.0%; Pred. No. 3e-122; Live 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5188643"
/clone_lib="NIR_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                            852 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI762690.1 GI:15754256
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BI762690
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Matches 679; Conserv
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BI762690
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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EST 29-FEB-2000
                                                                                                                      /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECo RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive
                                                                                                                                                                                                                                 hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-132881, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1347 AGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGG 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1407 AACGACCAGCGCTGCAAAACCCGAAACCGTTACATCTGCCCAGTTTGCCCAGGAGCACATC 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCCACA 1586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1767 AAAAAGGCTGCTCTTCCACCTGGCCCAGACCCTGTGGGGCAGCGGAGCTTCCCTGTGG 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1227 TICTGGATCGGGCTCACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAG 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1287 CACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTG 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 CAGGGAGGCCAGTGAGGGCCAGGGAGTGATAGAAGAAGCTGGGGCCCTTCGCCTGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 TITIGATIGGGAAGAIGGGCTICAAITAGAIGGCGAAGGAGGAGGACCGCCAGIGGICC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 AACGACCAGCGCTGCAAAACCCGAAACCGTTACATCTGCCAGGTTTGCCCAGGAGCACTACT
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704 bp mRNA linear EST 29-FEE
DKFZp434F2413_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434F2413 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 CACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGGAGGCCAGTGAGGGCCAGGGAGTGATTAGAAGAAGCTGGGGCCCTTCGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2055669"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                             Score 580; DB 9; Length 617;
Pred. No. 3e-120;
0; Mismatches 0; Indels 2
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/organism="Homo sapiens"
                /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                179 g
                                                                                                                                                                                                                                                                                                                              Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                      30.9%;
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Matches 617; Conservative
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI307814 617 bp mRNA linear EST 08-APR-1999 tb28d11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055669 3' similar to TR:061830 Q61830 MANNOSE RECEPTOR, C TYPE 1 PRECURSOR;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCC 360
                                                                                                                                                                                                                                                                    TITGIIGAAGI-GGICAGCCIAIGGIIIGCAGAGGGGCAGCGGIACAGCCACGCGG-CAG 537
                       256 CCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCC 315
                                                                                                                                                      241 CCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        597 AGCCAGCTGGGCTGTGGGCGGCACCT - GTGCTCTGCAGGCCAGACAGCGATAGAAGCCT
                                                                                                                                                                                                                                                                                                                                     181 TCCTTGGCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGCTCCGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGGCGCACCCTGCAAGTGGGGCTGGAACATGCAGCTG-CTGCCCGCGGGCTTGGCGTCC
    655 TIGICIGIGCCIACICCCCGGAGGCAACIGGGAGGICAACGGGAAG 701
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Insert Length: 725 Std Error: 0.00
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High quality sequence stop: 451.
Location/Qualifiers
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Unpublished (1997)
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AI307814
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AI307814/c DEFINITION

LOCUS

RESULT 11

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ORGANISM

SOURCE

ACCESSION VERSION KEYWORDS AUTHORS TITLE

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COMMENT

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                                                                                   δλ
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                                                                                                                                                                                                                                                                                                     Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 704)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
                                                                                                                                                                                                                                                                                                                                                                         sl sequence also available.
This clone (DKFZp434F2413) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                            This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGTGCGTCTGTGACATCGGCTACGGGGGGGCCCAGTGTGCCCACCAAGGTGCATTTTCCC 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1017 ITCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTC-AGAGGCAGA 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1076 CACCTATTACAGAGCCAGGATGAAATGTCAGAGGGAAAGGCGGGGGTGCTGGCCCAGATCAA 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 GICTGCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTAT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    717 AAGAAGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777 GACCATGCAGGGGGTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAAC 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CACGGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCTGGCTACACGGGCAGA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKF2p434F2413"
/clone_lib="434 (synonym: htes3)"
/tssue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 579.8; DB 9; 97.1%; Pred, No. 3.4e-120;
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0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                 AL040183.1 GI:5409148
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BF057185 612 bp mRNA linear EST 16-OCT-2000 7k17b07.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3444444 3 similar to SW:MANR_HUMAN P22897 MACROPHAGE MANNOSE RECEPTOR PRECURSOR. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ACCESTINCT: TOTATO TO THE TRANSPORT (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 181 c 179 g 135 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 612)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
1136 GAGCCAGAAAGTGC-AGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACG 1194
                                                                                                            1195 AGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCG 1254
                                                                                                                                                                                                                           1255 CCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTG 1314
                             1227 ITCTGGATCGGCTCACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAG 1286
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/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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Seq primer: -40UP from Gibco
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Tissue Procurement: Dr. Jöse Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 744)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                      1287 CACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCTGACACCACGGGCTGGTGTGGCGG 1346
                                                                                                                                                                        1347 AGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGG 1406
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                                                                                                                                                                                                                                                                                                   ACAACCAGCGCTGCAAAACCCGAAAACGTTACATCTGCCAGTTTGCCCAGGAGCACTC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 CACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCCAGGTTAAGACCACA 280
                       612 TTCTGGATCGGGCTCACCTACAAGACGGCCAAGGACTCCTCCCGCTGGGCCACAGGGGAG 553
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1827 CATGAACCCCACGGGGTATTAAATTATGAATCAGCTGAA 1865
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Unpublished (1997)
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BQ006636/c
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/dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//deb_host="Digner | Left Pethvis; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: Left Pethvis; Vector: pT7T3-Pac (Pharmacia)
//deb_host="Digner | Left Pethvis; Vector: pT7T3-Pac (Pharmacia)
//dep_host="Digner | Left Pethvis; Vector: pT7T3-Pac (Pharmacia)
//dep_host="Digner | Left Pethvis; Vector: The library was
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oilgo-dry primer containing a
Not I site. Double stranded cDNA was ligated to an ECOR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector: The oilgonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
//dep_located library is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1476 GGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTC 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1536 TGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATG 1595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1416 CGCTGCAAAACCCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGG 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1236 GGGCTCACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCC 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 GGAAGATGGGCTTCAATTAGATGGCGAAGGAGGACACCGCCAGTGGTCCAAAAAGGCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 ----GGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAG 468
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/tissue_type="Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUE=chondrosarcoma
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                          /clone="IMAGE:5846275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_SEQ=ACACTTGCAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 g
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Matches 613; Conservative
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                                                                                                      xs48f01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2772889 3' similar to SW:MANR_HUMAN P22897 MACROPHAGE MANNOSE RECEPTOR AW299257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: Kidney; Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following Happurification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneDS 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 611)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Bamall: gapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227 ITCTGGATCGGGCTCACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAG 1286
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  /clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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/clone="IMAGE:2772889"
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Unpublished (1997)
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1527 CACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCCAGGTTAAGACCACA 1586
                                                                             1707 ITTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGGACACCGCCAGTGGTCC 1766
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                                                 1827 CATGAACCCCACGGGGTATTAAATTATGAATCAGCTGA 1864
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Search completed: December 28, 2002, 20:45:31 Job time : 2518.87 secs us-09-944-896-49.rni

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Sequence 1, Appli
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7664.697 Million cell updates/sec
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Sequence 14,
Sequence 21,
                                                                                                                                                                                 December 28, 2002, 16:48:37; Search time 75.0618 Seconds
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Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-387-942C-18

US-08-387-942C-1

US-08-404-665-3

US-08-404-671-3

US-08-404-781-3

US-08-404-781-3

US-08-404-781-3

US-08-404-781-3

US-08-404-781-3

US-08-387-942C-17

US-08-387-942C-21

US-09-387-942C-21

US-08-387-942C-21

US-08-387-942C-21

US-08-387-942C-21

US-08-387-942C-21

US-08-387-987-1

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 2000000000
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Match Length DB
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Seguence	Sednence	Sedneuce	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence
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                    Sequence 321, Application US/09404879A

Sequence 321, Application US/09404879A

Patent No. 6468546

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER.
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION UNMBER: US/09/404,879A

CURRENT FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastsEQ for Windows Version 3.0

LENGTH: 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCTTTGTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904 AAGIGAGGIGCAGCCIGCAGIGIGIGCACGCCGGCIICCGGGAGGAGGAGTGCTCGTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 672.8; DB 4;
Pred. No. 4.2e-162;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(690)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.33
Matches 685; Conservative
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-404-879A-321
              US-09-404-879A-321
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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RESULT 1
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Sequence

Sequence Sequence Sequence

Sequence Sequence

US-09-688-307A-1 US-08-485-618-98 US-08-605-672-98 US-08-482-293A-98

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TCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACAAGGTGCATTTTCCCTTCCACA 1023
                                                                                                1024 CCTGTGACCTGAGGATCGACGGAGCTGCTTCATGGTGTCTTCAGAGGCAGACCCTATT 1083
                                                                                                                                                       1084 ACAG-AGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1142
                                                                                                                                                                                                              1143 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGCCACCAACGAGGTGACT 1202
                                                                                                                                                                                                                                                                    1203 GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC 1262
541 AAAGIGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 600
                                                                                                                                                                                                                                                                                  APPLICANT: Famedu, Omolayo O.
APPLICANT: Han, Feng
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Disease Resistance Factors
FILE REFERENCE: BB1252 US NA
CURRENT APPLICATION NUMBER: US/09/433,248A
CURRENT FILING DATE: 1999-11-04
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
LENGTH: 582
                                                                                                                                                                                                                                                                                                                              TCCTTCCGCTGGGCCACAGGGGAGCACCAG 1292
                                                                                                                                                                                                                                                                                                                                            661 TCCTTNCGCTGGGCCACAGGGGACCAG 690
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09433248A Patent No. 6355462
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unsure (370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unsure (421)
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(481)
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(484)
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(502)
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(547)
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NAME/KEY:
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                                                                                                                                     1210 ACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGACTCCTTCC 1269
                                                                                                                                                                                                                     1270 GCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCTGACAACC 1329
                                                                                                                                                                                                                                                                                                                              61 GGCAAGCCATCGGCACACGTGGAGCGCCATCTTCGGGTGGCTCGCGCGCCCAACG 120
                                                                                                                                                                          1 ACATCCTGAACCGGACCATCGCCATGGACACCTCCAACAAGGCCACCTCCGACTACGTCC 60
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49.8%; Pred. No. 0.081;
tive 0; Mismatches 111; Indels 0
                                                       Length 582;
                                                   Score 47.8; DB 4; Length 5 Pred. No. 0.0047; 0; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/387,942C FILING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1809-106P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08387942C Patent No. 599289
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVETN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                     2.5%;
50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
                                                   Query Match 2.55
Best Local Similarity 50.27
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 110; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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Best Local Similarity
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STATE: VA
COUNTRY: USA
22042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-387-942C-18
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US-09-433-248A-3
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1016 CTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTTCTAGAGGCAGA 1075

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US-08-387-942C-1
                                                                                                                               1136 GAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGA 1195
                                                        1076 CACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAA 1135
357 CGGCTGGTTCAACGGCTACATCCCCGGCCAGGACGCCCCGATCGCGACGTGACCCTGGA 416
                                                                                                                                                      TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           1196 GGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCG 1236
                                                                                                                                                                                                                             ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O.BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Azotobacter vinelandii
STRAIN: E
                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08387942C
Patent No. 5939289
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ERTESVAC, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LAKESN, BJORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INPULOGY: linear MOLECULE TYPE: DNA (genomic) ORGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
6702..9695
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9973..12588
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2227..6438
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CITY: FALLS CHURCH
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LOCATION:
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                                                                                                                                                                                                                                                                                                                     US-08-387-942C-1
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                                                                                    1016 CTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGA 1075
                                                                                                          2523 CTTCGGCATGAGCGACCTGACCCTCGACGGCAACCGCGACACCTGTCCGCCAAGGTCGA 2582
                                                                                                                                                                      1076 CACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAA 1135
                                                                                                                                                                                                2583 CGGCTGGTTCAACGCCTACATCCCCGGCCAGGACGCCCGATCGCGACGTGACCCTGGA 2642
                                                                                                                                                                                                                                                          1136 GAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAAGGA 1195
                                                                                                                                                                                                                                                                                                  2643 GCGGGTGGAAATCCGCGAGATGTCCGGCTACGGTTTCGACCCCCACGAGCAGACCATCAA 2702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          944 GGAGGAGGAGTGCTCGTGTGTGACATCGGCTACGGGGGGAGCCCAGTGTGCCACAA 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1004 GGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTC 1063
    Length 12588;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99; Indels
                                       0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9503747
Sequence 1, Application.
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
                                                                                                                                                                                                                                                                                                                                              1196 GGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCG 1236
                                                                                                                                                                                                                                                                                                                                                                     2703 CCTGACGATCCGCGACGACGACACACACCTCG 2743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; Score 42.6; DB 5; 53.0%; Pred. No. 0.19;
  DB 2;
Score 43.4; D. Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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CLASIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: F9-
TELECOMMUNICATION INFORMATION:
  2.3%;
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                          Conservative
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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112..2848
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CITY: San Diego
STATE: California
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Query Match
Best Local Similarity
Matches 110; Conserv
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PCT-US95-03747-1
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PCT-US95-03747-1
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COUNTRY:
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2166 CCTCCACTTCTGCAGCCCCGGTTGGGAC---GCCTTCCAGGGTGCCTGCTACAAGCACTT 2222
                                                        1064 TTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGGAAAGGCGGGGTGCT 1123
                                                                                   1047 GTTTGGCAAGAATTGCTCGGAGCCCTACTGCCCGCGGGTTGCTCCAGCCGGGGGGTGTG 1106
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                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                 2283 GGCCAGCATCAGCACGCGGAGGAACAGGACTTCATC 2319
                                                                                                                                        1124 GGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTC 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/404,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: FUGIT, DONNA R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3341
                                                                                                                                                                                                                                                                                Sequence 3, Application US/08404665
Patent No. 5591583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08404671
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Best Local Similarity 52.38
Matches 90; Conservative
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EDNESS: double
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CLASSIFICATION: 435
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US-08-404-671-3
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987 CIGCAGIGGCCACGGCAACTITAGCITIGAGTCCIGIGGCIGCATCTGCAACGAAGGCIG 1046
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APPLICANT: Reid, Robert A.
APPLICANT: Hemperly, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: BUGNES:
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
STREET: L Becton Drive
CITY: Franklin Lakes
STATE: NUMBER OF STATE: NUMBER OF STATE:
                  GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: SEQUENCES
                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
STREET: I Becton Drive
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: FUGIL, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4724 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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STRANDEDNESS: double
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Patent No. 5635360
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US-08-232-463-14/C
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Sequence 17, Application US/08387942C

GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: BROODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O.BOX 747
COTTY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                              Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.63
0; Mismatches
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                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,781 FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: MRRHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION:
                                                                                                                                                                                                                                              NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P--
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4724 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.39
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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US-08-404-781-3
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OTHER INFORMATION: "n" bases at various positions throughout the sequence CTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                  1133 CAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTTCTATCTGGGCCGCCTGGAGCCACCAA 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007 000
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                        Length 1176;
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                                                                                                                                                                                                                                                                                        Query Match 2.1%; Score 39.4; DB 2;
Best Local Similarity 52.1%; Pred. No. 0.85;
Matches 88; Conservative 0; Mismatches 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09103840A Patent No. 6294328
                                               INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
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US-09-103-840A-2/c
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                              TELEFAX:
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1142 RRRRRRRRRRRRRRRR 1124

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1558 TCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTG 1617
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                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29,768
3R: 30472/114 IMMU
                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
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TELEX: 899149
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1858 CAGCTGAAAAAAAAAA 1876
                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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US-08-232-463-14
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1076 CACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAA 1135
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Similarity 48.4%; Pred. No. 1.3;
                                                                                                        APPLICANT: ERESVAG, HELGA
APPLICANT: VALLA, SYEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LAREEN, BJOK RUDMUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEB: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 114; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/387,942C
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....ек: US/08/387,942С
09-MAY-1995
ти: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEBRAX: 703-205-8050
                                        Sequence 21, Application US/08387942C Patent No. 5939289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
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; Sequence 9, Application US/09387574
; Patent No. 6168951
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
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                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                   STATE: VA
RESULT 12
US-08-387-942C-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0%; Score 37.4; DB 4; Length 2335; Best Local Similarity 51.5%; Pred. No. 3.5; Matches 86; Conservative 0; Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1301 CAGTITIGCCTTIGGGCAGCCIGACAACCACGGGCIGGTGTGGCTGA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1301 CAGTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGGGCTGA 1347
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Tony
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Geranylgeranyl Transferases
FILE REFERENCE: BB1239 US NA DIV
              APPLICANT: Kinney, Tony
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Geranylgeranyl Transferases
FILE REFERENCE: BB-1239
CURRENT APPLICATION NUMBER: US/09/387,574
EARLIER APPLICATION NUMBER: 60/098,743
EARLIER PILING DATE: September 1, 1998
NUMBER OF SEQ ID NOS: 12
SORTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/668,096
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/098,743
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 09/387,534
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09668096
Patent No. 6312954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsoft Office 97
APPLICANT: Cahoon, Rebecca E.
                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-387-574-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Oryza sativa
US-09-668-096-9
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                                                                                                                                                                                                                                                      SEQ ID NO 9
LENGTH: 2335
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APPLICANT: Lerman, Michael I.
APPLICANT: Lerman, Michael I.
APPLICANT: Lerman, Michael I.
APPLICANT: Lerman, John D.
APPLICANT: Heatif, Farida
APPLICANT: Sekido, Yoshitaka
APPLICANT: Sekido, Yoshitaka
APPLICANT: Buh, Fuh-Mei
TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
CURRENT APPLICATION NUMBER: US/09/470,443
CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 60/114,359
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 CIGCAAGTGGGGTTGGAACATGCAGCTGCTGCCGGGGCTTGGCGTCCTTTGTTGAAGTG 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 GCCAGGGCAGCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGGGGCACC 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.0%; Score 37.2; DB 4; Length 1070;
46.0%; Pred. No. 3;
tive 0; Mismatches 148; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 GGGCGCCACCTGTGCTCTGCAGGCCAGACAGCGA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: December 28, 2002, 21:15:21
                 Sequence 7, Application US/09470443
Patent No. 6441156
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.09
Matches 126; Conservative
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                        This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532) coding for human PRO347 (UNO366) (see AAY06482). The clone was isolated from a foetal kidney library. Amplification of DNA44176 occurs in various tumours, suggesting an association with tumour formation or growth. Antagonists (e.g. antibodies) directed against PRO347 may have use in cancer therapy. The invention identifies 14 genes (see AAX8724-67) that are amplified in the genome of tumour colls. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of
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                                                           Hillan KJ,
                                                           Gurney AL,
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98US-0088742.
                                                           Goddard A,
                                    (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                           The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-prolliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1326; DB 20; Length 1876; 100.0%; Pred. No. 7.8e-299;
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                                                                                                                                                                                                                                                                                       Nucleic acids encoding PRO secreted and transmembrane
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                                                                                                                                                                                                                            Gurney AL,
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                                                                                                                                                                                                                                                                                                           Claim 2; Fig 22; 123pp; English.
                                                                                                                                                                                                                           Baker KP, Chen J, Goddard A,
                                                                  970S-0069334.
970S-0069335.
970S-0069425.
970S-0069694.
                                                                                                                                        97US-0069873.
97US-0068017.
98US-0070440.
98US-0074086.
                                       98US-0075945
                                                  97US-0067411.
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97US-0069870
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                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                          WPI; 1999-371118/31.
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                                                                  11-DEC-1997;
11-DEC-1997;
12-DEC-1997;
16-DEC-1997;
16-DEC-1997;
17-DEC-1997;
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18-DEC-1997;
05-JAN-1998;
09-FEB-1998;
10-JUN-1999
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                                                                                                                GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG
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TGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGGGGCCACCTCAAGCCAG
                                                                                                                                                                                                                                                                                                                                GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT
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                                           TGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGGGCCACCTCAAGCCAG
                                                                                            CTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGT
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PRO1112, PRO509, PRO883 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth
                                                                  SS
                                                                                                                                                                                                                                                                                                                                                                                                                  anti-polypeptide antibody useful in the treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCCCTGCACACCGCCTGCGCAGC 180
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                                       PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1326; DB 21; Length 1876; 100.0%; Pred. No. 7.8e-299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                            cell growth and proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                     encoding novel polypeptide PRO347.
                                                                                                        Location/Qualifiers
123..1490
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 50; Fig 13; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferation in mammals.
                                                                                                                                                                                                                              99WO-US05028.
99WO-US12252.
99WO-US20111.
                                                                                                                                                                                                                                                                       99WO-US28313.
                                                                                                                                                                                               99WO-US30095
                                                                                                                                                                                                                     98US-0113296
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(first entry)
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                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                 2000-452188/39.
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                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY93690
                                                                                                                                                     WO200037640-A2
                                                                                     Homo sapiens
                                                                                                                                                                                                                              08-MAR-1999;
02-JUN-1999;
01-SEP-1999;
15-SEP-1999;
                                                                                                                                                                                             16-DEC-1999;
03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                 Botstein D,
Wood WI;
                                                                                                                                                                                                                                                                       30-NOV-1999
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                                                                                                                                                                                                                   22-DEC-1998
                                                                                                                                                                                                                                                                                            01-DEC-1999
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963 GTCTGTGACATCGGCTACCGGGGAGCCCACTGTGCCACCAACGTGCATTTTCCCTTCCCT 1022
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1383 CAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACATC 1442
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This represents the coding sequence of the human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 colns insert is deposited with ATCC under accession number 98694. The T139 polypeptides and polymorlocides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant T139 expression or activity, especially proliferative or modulate spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat disorders related to defects in sperm-egg fusion. They may also be useful to treat testicular disorders e.g. binding compounds which may be useful for detecting the polypeptides in for detecting the polypeptides in for detecting the polypeptides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         samples; and identifying compounds modulating polypeptide activity. The polynuclectides are useful for producing probes or primers that selectively hybridize to the polynuclectides which may be useful for detecting the polynuclectides in a sample, gene mapping; identifying cells or tissues expressing aberrant T139 levels; determining if a gene max been mutated or deleted to identify subjects at risk for or having a disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; T139 polypeptide; immune system disorder; spermatogenesis; ss; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
                                                                                                   1323 GACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG 1382
                                                                                                                                                                                    1383 CAGGCTTCAGCTGCCTTCAACTGGAACGACCGCTGCAAAACCCGAAACCGTTACATC 1442
1141 TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCT 1200
                                                                             GACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG 1260
                                                                                                                                                               CAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAAACGGTTACATC 1320
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                   1163 TCCTTCGCTGGGCCACAGGGAGCACCAGGCCTTCACCATTGGGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human T139 protein coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                          AAZ23300 standard; cDNA; 1338 BP.
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961 TACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
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                                                                                                                  1 ATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC
                                                                                                                                              1 ATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC
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therapeutic administration to modulate/prevent T139 expression
                                                    Score 1254; DB 20; Length 1338;
Pred. No. 4e-282;
0; Mismatches 5; Indels 27;
                           Sequence 1338 BP; 259 A; 420 C; 413 G; 246 T; 0 other;
                                                      Query Match 94.6%;
Best Local Similarity 97.6%;
Matches 1294; Conservative
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cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; malematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/product= "Mature human protein with hydrophobic domain"
1260
                                                                                                                                                                                                                                                                   1320
                                                                                              GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC 1140
                                                                                                                                                                                                                                                                             1234 CAGGCTTCAGCTGCCTTCAACTGGAACCAGCGCTGCAAAACCCGAAACCGTTACATC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein having hydrophobic domain encoding cDNA clone HP10760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
                                                         AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT
                                                                                                                                                   TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCCTTTGGGCAGCCT
                                                                                                                                                                 1141 TCCTTCCGCTGGGCCACAGGGAGCACCAGCCTTCACCAGTTTTGCCTTTGGGCAGCCT
                                                                                                                                                                                                          GACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTTGGCAACTGCGTGGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; hydrophobic domain; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  AAD12570 standard; cDNA; 1775 BP
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(SAGA ) SAGAMI CHEM RES CENT.
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                                                                                                                                                                                                                                                                                                                     1321 TGCCAG 1326
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11-JAN-2000;
03-FEB-2000;
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The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10760. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides associated with inappropriate polypeptide express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional complements, to modulate cytokine and cell proliferation activity, to modulate of microbial infections and autoimmune disorders such as multiple sclerosis, remunestantial autoimmune disorders such as multiple sclerosis, themmatodiate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's catement of Parkinson's disease, Huntington's disease and Alzheimer's disease, to modulate activity and inhibin activity, to modulate receptor condulate themostatic and thrombolytic activity, to modulate receptor controlling activity, to modulate haemostatic and thrombolytic activity, to modulate receptor controlling activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                  Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
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                                                                                                                                                                                                   Claim 4; Page 271-275; 563pp; English.
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97.68;
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                                                       WPI; 2001-418355/44.
                     Kimura T;
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                                                                              P-PSDB; AAE06575
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Matches 1294;
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                     Kato S,
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Human; T139 polypeptide; immune system disorder; spermatogenesis; ss; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
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                                                                                                                                                                        601 GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT
                                                                                                                  GCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA
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                                          541 GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG
                                                                     602 GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG
                                                                                                                                                                                                                                             782 GGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC
                                                                                                                                                                                                                                                                          CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGGAGTGCTCGTGC
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expressed by standard recombinant methodology. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 cDNA insert is deposited with ATCC under accession number 98694. The T139 polypeptides and polynucleotides can be administered therapeutically or reat/prevent disorders associated with aberrant T139 expression or activity, especially proliferative or differentiative captured specially proliferative or differentiative captured specially of the immune system. They can be used to modulate spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat disorders related to defects in sperma-egg fusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively binding compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating polypeptide activity. The polynucleotides in compounds modulating polypeptide activity. The polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant corresponds to a sample, gene mapping; identifying cells or tissues expressing aberrant corresponds or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic interventions; and for producing antisense sequences for therapeutic interventions; and for corrections and for producing antisense sequences for therapeutic interventions; and for corrections and for producing antisense sequences for therapeutic interventions; and for corrections and for producing antisense sequences for therapeutic interventions; and for producing antisense sequences for therapeutic interventions.
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Pred. No. 4.4e-282;
0; Mismatches 5; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;
                                                                                   /*tag= a
/product= "T139 protein"
                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                        Location/Qualifiers
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Best Local Similarity 97.6
Matches 1294; Conservative
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  Homo sapiens.
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                                                            CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC
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Human; haematopoiesis; clotting; kidney failure; wound healing; cancer; neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease; heart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive; glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; gynaecological; haemostatic; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; antibacterial; organication; antidiabeltic; cerebroprotective; tranquilliser; appoptotic disorder; rheumatoid arthritis; cardiant; renal disorder; appoptotic disorder; rheumatoid arthritis; cardiant; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular profiterating discrete
                                                                                                                                                                                                                                                                                           nepatotropic; antipsoriatic; antiallergic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ. ID. NO. 3 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c /product= "Human mature T139 protein" 95..1432 /*tag= d /note= "This region designated as SEQ specifically referred in claim 27"
                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Human T139 protein"
95..172
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                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                         AAD33531 standard; cDNA; 1856
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98US-0102705.
98US-0124538.
99US-0298531.
99US-0337930.
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                                                                                                           Human T139 (TANGO-139) CDNA.
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22-JUN-1998;
29-JUL-1998;
23-APR-1999;
22-JUN-1999;
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The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-139), T125 or murine WDNM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability to modulate colotting. Polypeptide and polypeptide of the invention are useful interactions, antibodies are useful as modulating agents in regulating and treating disorder characterised by their aberrant expression or activity. The callular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful for treating kidney defects such as kidney failure, TANGO-135 is useful in wound healing and for treating cancer, TANGO-110, is useful for treating healing and for treating cancer, TANGO-110, is useful for treating neoplasia, TANGO-177 or WDNW-2 is useful for treating neoplasia, and tumours, and injury or trauma to the brain. TANGO-125, 110, 175 and injury or trauma to the brain. TANGO-125, 110, 175 and injury or treating cancer TANGO-139, 125, 110, 175 and injury or treating cancer TANGO-139, 125, 110 and 175 molecules are useful to treat cheart disease, cardiovascular disease, such as ischaemic heart disease. TANGO-139, 125, 110 and 175 molecules are useful to treat chronic glomerulonephritis), TANGO-175 is useful to treat uterine correct fideway) disorders, such as inflammatory diseases and dimmous. TANGO-175, or treating proliferative disorders, such as inflammatory diseases and disorders, such as inflammatory diseases and disorders, inflammatory disorders. TANGO-175, or WDNW-2 activity also include apoptotic disorders, rhementoid arthitis, inflammatory disorders, wirell munors. TANGO-175, en immune-related disorders, inflammatory disorders, viral, immune-related disorders, inflammatory disorders, viral, immune-related disorders, inflammatory disorders, viral immune related disorders, e.g., immunodeficiency disorders, viral disorders, cell growth disorders, e.g., cancers and inflammatory disorders and apoptotic disorders. The nucleic acids of the invention are used in gene therapy. The present sequence is human T139 cDNA. CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC 120 121 GGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCCTGCACCGCCTGCGCAGC 180 240 241 CTGGCTCAAGCCAGGCCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG 300 420 TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCCTTT 360 9 454 27; Gaps 1 ATGCTGCATCCAGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCTC TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA CTGGCTCAAGCCAGGCCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCGTCCGGCCTG GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAG 94.6%; Score 1254; DB 24; Length 1856; 97.6%; Pred. No. 4.4e-282; .ive 0; Mismatches 5; Indels 27; Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other; Matches 1294; Conservative Best Local Similarity Query Match 61 395 335 301 361

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1321 TGCCAG 1326
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                                 CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC 780
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541 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG
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Young F
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                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 26 human secreted polypeptides, preventing, diagnosing and/or treating cancers and for
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(A, Ni J,
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Florence KA,
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0; Mismatches
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                                                                                                                                                                                                                                                   Ebner R,
                                                                                                                                                                                                                               Duan RD,
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Best Local Similarity 97.6%;
Matches 1294; Conservative
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                                                                                                                                             99US-0137725
                                                                                                   02-JUN-2000; 2000WO-US15187
                                                                                                                                                                                                                            Birse CE, D
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                 WO200075375-A1
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                                               GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCCTATAAGAAG
                                                                           GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT
                                                                                                                                                                                                                                           GCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                            830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation ^{\circ}
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T, Koqa
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Pred. No. 3.1e-280;
0; Mismatches 10; Indels 27;
                                                                                                                                                                                                                                                                                         8; SEQ ID NO 2850; 1380pp + sequence listing; English.
                                                                                                                                                                                S, Otsuki
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                                                                                                                                                                   Ishii S,
                                                                                                                                                                   ni T, Hayashi K,
Nagai K, Kojima
                                                                                                                                                                Nishikawa T, Isogai T,
                                                                               99JP-0194486.
2000JP-0118774.
2000JP-0183765.
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Best Local Similarity 97.2%;
Matches 1289; Conservative
                                                   07-JUL-2000; 2000EP-0114089
                                                                                                                                                                              Wakamatsu A, Sugiyama T,
                                                                                                                                      (HELI-) HELIX RES INST.
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                    CGTCTCAACATCAGCACCTGCCACTGTCCCCCTGGGTACACGGGCAGATACTGC 780
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                                                                                         GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT 660
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481 CTGGGCTGTGGGCGCCCCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGT
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as companient. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in classonsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and answers.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.9%; Score 1205.6; DB 23; Length 1934; 95.9%; Pred. No. 8e-271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 27594; 103pp; English.
                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                            30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                           Liu C,
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                                      GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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                                                                                                                                                           DNA encoding novel human diagnostic protein #12148.
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Pred. No. 2.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 12148; 103pp; English.
                                        BP.
                                     AAS76344 standard; cDNA; 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT;
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                                                                                                                                                                                                                                                              Homo sapiens
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                                                                             AAS76344;
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                                                                                       CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC
                                                     307 CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAACCCCCAACCCCGAGCCTGGCGTCCGGCCTG
                                                                           TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGGCTTGGCGTCCTTT
                                                                                                                      GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAG
                                                                                                                                                                 TGTGCTCGCAACGCCACCTGCACCACTACACGCACCTCGTGGGCCCACCTCAAGCCAG
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                                241 CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG
                                           Human ovarian carcinoma antigen polynucleotide SEQ ID NO:321.
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RESULT 14
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                                                                                                                                                                                                                                                                                                            The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                 treatment of
           Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGCTGTGGGCGGCACCTGTGCTGCAGGCCAGACGATAGAAGCCTTTGTCTGTG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 CCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGG 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment cancer, preferably ovarian cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.7%; Score 672.8; DB 21; Length 690; Best Local Similarity 99.3%; Pred. No. 5.4e-147; Matches 685; Conservative 0; Mismatches 4: Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
                                                                                                                                                                                                          Algate PA, Frudakis TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 5.4e
0; Mismatches
                                                                                                                                                                                                                                                                                           Claim 1; Page 177; 299pp; English.
                                                                                                                                        98US-0216003.
99US-0338933.
99US-0404879.
                                                                                                          99WO-US30270
                                                                                                                              98US-0215681
                                                                                                                                                                                                      Mitcham JL, King GE,
                                                                                                                                                                                                                             WPI; 2000-431589/37.
                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                               WO200036107-A2
                                           Homo sapiens.
                                                                                                        17-DEC-1999;
                                                                                                                              17-DEC-1998;
                                                                                                                                         17-DEC-1998;
                                                                                                                                                           24-SEP-1999;
                                                                                                                                                  23-JUN-1999;
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Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer -
                                                                                             962 ACAG-AGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
                                                                                                                                                                                                                                                                                     1081 GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to polypeptides comprising an immunogenic portion of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an
Fanger GR;
                                                                                                                           1021 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT
                                                                                                                                                                                                                      601 GACAGTGACTTTGAGACCAGGAACTTCTGGATNGGGCTCACCTACAAGACCGGCAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunostimulant; cytostatic; cancer; ovarian carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response in a patient and treating ovarian cancer. This sequence represents DNA related to the invention.
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Pred. No. 5.4e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retter MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fling SP, Retter
Hill P, Albone E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovarian carcinoma antigen polynucleotide #9.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 661 TCCTTNCGCTGGGCCACAGGGGAGCACAG 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 296; 408pp; English
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Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0617747.
2000US-0636801.
2000US-0667857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN72904 standard; DNA; 690
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18-JUN-2001; 2001US-0884441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2002 (first entry)
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Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-164781/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps

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Indels

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ACAG-AGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
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                                                                                                                                                                                                                                                                               360
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                                                                                                                                                                                                                                                                                                                     CCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCATCCCCTATAAGAAGG 601
                                                                                                   GTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATG 661
                                                                                                                                                   CAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGAC 721
            1 TGGGCTGTGGGGGGGCACCTGTGCTCTGCAGGCCAGACGGATAGAAGCCTTTGTCTGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                    241 GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCC
                                                                                                                                                                                                                                                                      CCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACTATT
                                                                                                                                                                                                                                                                                                                                                                      181 CAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGAC
                                                                                                                                                                                                                                                                                                        TCTGTGACATCGGCTACGGGGGGGGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA
482 TGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTG
                                                                                                                                                                                                      GTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCC
                                                                                                                                                                                                                                                        AAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #12147.
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23-AUG-2000; 2000US-0649167
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The invention relates to isolated polynucleotide (I) and peptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The card gene mapping, and in recombinant production of (II). The complete are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of and to produce other types of data and products dependent on DNA and amino acid sequences. Ass64197-AAS94564 represent novel human cid sequence data for this patent did not appear in the printed of sequence data for this patent did not appear in the printed of sequence obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 TGTGCTGGCAACGCCACCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCTCCTGCACAACCGCCTGCGAGC
                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 49.6%; Score 657.2; DB 23; Length 906; Best Local Similarity 95.3%; Pred. No. 2.5e-143; Matches 688; Conservative 0; Mismatches 33: Tadala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 906 BP; 175 A; 294 C; 286 G; 151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 12147; 103pp; English.
                                                         Tang YT;
                                                         Drmanac RT, Liu C,
                                                                                               WPI; 2001-639362/73
                   (HYSE-) HYSEQ INC.
                                                                                                                         P-PSDB; ABG12156
                                                                                                                                                                                                                           biodiversity
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Οy	481	CTGGGCTGTGGGCGCCACCTGTGCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGT	540
qa	209	CTGGGCTGTGGGCGCGCCCTGTGTTTTTTTTTTTTTTT	999
Qy	541		009
QQ	299	GCCTACTCCCCCAGAGGCAACTGGGAGGTCAACGGGAAGACAATCGTCCCCTATAAAAAG	726
δλ	601	601 GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT	099
qq	727		786
QY	661		719
QQ	787		846
Qy	720	AC 721	
QΩ	847	 847 AC 848	

Search completed: December 28, 2002, 17:01:44 Job time: 271.586 secs

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(without alignments)
11372.097 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		The state of the s	CDNA CLONE encodin	Human PRO347 nucle	CLINA encoding nove	Human PRO347 CDNA.	Human Protease and	DNA encoding novel	Human T139 protein	Human protein havi	naman 1139 procein
SUMMARIES		ID			AAX80053	AAA46918	AAA49561	AA750925	AAS76343	AAZ23300	AAD12570	AAZ23299	
		DB	į	20	20	21	21	15	23	20	22	20	
		Length	1 1 1 1 1 1	1876	1876	1876	1876	855	906	1338	1775	1856	
de	Query	e Match Length DB]	1 1 1 1 1 1 1	100.0	100.0	100.0	100.0	4.66	99.4	99.4	99.4	99.4	
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05-JAN-1998; 29-APR-1998; 22-MAY-1998;

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24 AAD33531 22 AAF24152 22 AAH98469 22 AAK91830 22 AAK93233 22 AAK93246 33 AAS91790	AAS763 AAS763 ABL577 AAH050 AAH986		22 AAD17764 22 AAD17766 22 AAD17767 24 AAD38692 24 AAL39682 22 AASG0871		3 AAS75116 9 AAV42646 2 AA160658 0 AAX52263
	9840 939 939		100 112 112 112 336 377		047 970 803 875
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10 11 12 13 14 16	11 12 12 13 13 14	222 222 223 205 205 205	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 4444 4444 75

ALIGNMENTS

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PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human; ss.
                                                           cDNA clone encoding human PRO347, amplified in tumour cells.
                                                                                                           Location/Qualifiers
123..1490
              AAX87260 standard; cDNA; 1876 BP.
                                                                                                                                                                                                                    98US-0109304.
98US-0070440.
98US-0083500.
98US-0086414.
                                                                                                                                                                                                      99WO-US00106.
                                           27-SEP-1999 (first entry)
                                                                                                                          /*tag= a
123..200
/*tag= b
201..1487
/*tag= c
                                                                                           Homo sapiens,
                                                                                                                                                                     W09935170-A2.
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                                                                                                                                 sig_peptide
                                                                                                                                                 mat_peptide
                             AAX87260;
RESULT 1
      AAX87260
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10-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 GAGAGITICITICITICITICCCCCCCCACACCCCCTGCCCAGCTGCGTCCAGCCCCCTGCG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence of CDNA clone DNA44176 (ATCC 209532) coding for human PRO347 (UNQ306) (see AAY06482). The clone was closed from a feetal kidney library. Amplification of DNA44176 occurs in various tumours, suggesting an association with tumour formation or growth. Antagonists (e.g. antibodies) directed against PRO347 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX60477-90) may be useful targets for the diagnosis and/or treatment (including prevention)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGIGIGGCCACCCCAGCIGCAGGAGCAGGCICCGAIGGCCGGAGCCCIGAACAGGAAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder; ss.
                                                                                                                                             Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 100.0%; Score 247; DB 20; Length 1876; Conservative 0; Mismatches 0; Indels 0;
                                                                  Gurney AL, Hillan KJ, Lawrence DA;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO347 nucleotide sequence.
                                                                                                                                                                                          Example 1; Fig 13; 162pp; English.
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      98US-0088742.
                  98US-0107783.
                                                                      Goddard A,
                                            (GETH ) GENENTECH INC.
                                                                                                             WPI; 1999-430385/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                   Wood WI;
                                                                                                                                                                                                                                                                                                                                                                             tumour treatment
                                                                                                                           P-PSDB; AAY06483
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      10-JUN-1998;
10-NOV-1998;
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                                                                      Botstein D,
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                                                                                    ROY MA,
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transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes nucleic acids encoding PRO secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAGITICITGCICCICCTCCCTGCACAACCGCCTGCGCTGGGTCCAGCCCCTGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GAGAGTTTCTTGCTCCTCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 247; DB 20;
; Pred. No. 7.1e-51;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA46918 standard; cDNA; 1876 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 22; 123pp; English.
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97US-0068017.
98US-0070440.
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97US-0069870.
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98WO-US25108
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P-PSDB; AAY17828.
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01-DEC-1998;
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1026, PRO344, PRO343, PRO347, PRO1015, PRO1017, PRO1012, PRO509, PRO863 and PRO8082. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment, and diagnosis of neoplastic cell growth
                                                        PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                              New anti-polypeptide antibody useful in the treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAGITICITGCICCICTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 247; DB 21; Length 1876; 100.0%; Pred. No. 7.1e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         neoplastic cell growth and proliferation -
                                       cDNA encoding novel polypeptide PR0347.
                                                                                                                   Location/Qualifiers
123..1490
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 50; Fig 13; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and proliferation in mammals.
                                                                                                                                                                                                                                                                    99WO-US28409.
99WO-US28409.
99WO-US28301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%;
Matches 247; Conservative (
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                    (first entry)
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                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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                                                                                                                                                          WO200037640-A2
                  03-OCT-2000
                                                                                                Homo sapiens
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02-JUN-1999;
01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
                                                                                                                                                                                                16-DEC-1999;
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01-DEC-1999
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 AAA46918;
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New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical
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181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG 240
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO; membrane bound protein; secreted protein; PRO357; PRO343; PRO243; PRO715; PRO241; PRO323; PRO313; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human;
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,, Godowski PJ, Grimaldi CJ, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= PRO347 polypeptide
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123..1490
                                                                                                                                                                                                                                                                                                                   AAA49561 standard; cDNA; 1876 BP
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98US-0112850.
98US-0113296.
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Æ, Goddard A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO347 cDNA.
                                                                                                                 241 GGCTGGA 247
                                                                                                                                                                    441 GGCTGGA 447
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Gerritsen ME,
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Drmanac RT, Liu C,
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                    Protease and associated protein-9; PPRG-9; anti-PPRG antibody; diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder; AIDS; Addison's disease, adult respiratory distress syndrome; allergy; ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic; antiantlammatory; virucide; antipsoriatic; anti-HIV; antiallergic; immunosuppressive; antidiabetic; antianaemic; neuroprotective; human; ss.
                                                                                 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGGCGCACCCTGCAAGTG 240
                                                                                                                      201 GAGGTGTGGCCACCCCAGCTGCAGAGCTCCGATGCCCGGAGCCCTGAACAGGAAG 260
                                   GAGAGITICITGCICCICCICCTGCACAACCGCCIGCGCAGCTGGGICCAGCCCCTGCG 120
                                                     261 GAGAGTTTCTTGCTCCTCTCCCTGCACACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCG 320
                                                                        GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
9
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1 C, Au-Young J;
GAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG
                                                                                                                                                                                                                                                                   Human Protease and associated protein-9 (PPRG-9) encoding cDNA.
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Yue H, Tang YT, Reddy R, Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety= "Probe or Primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product= "Mature PPRG-9"
                                                                                                                                                                                                                                                                                                                                                                                                                 "Human PPRG-9
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                             AAZ50926 standard; cDNA; 855 BP.
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/product=
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311.730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY70015
                                                                                                                                                241 GGCTGGA 247
                                                                                                                                                          441 GGCTGGA 447
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
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Shih LL, L
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The present sequence is a cDNA identified in Incyte clone 998626 derived from KIDNTUT01 cDNA library. It encodes human protease and associated protein-9 (PPRG-9), which is expressed in urologic and musculoskeletal tissues. Anti-PPRG antibodies can be used as therapeutic antagonists, reagents for diagnosis and monitoring diseases and for isolating PPRG. PPRG nucleotide sequence can be used as probe or primer for diagnosis and monitoring of PPRG-related diseases and gene mapping. PPRG can be used in the treatment of cell proliferative disorders like cancer, arteriosclerosis, atherosclerosis, bursitis, cirrhosis and hepatitis, and immune disorders like AIDS, Addison's disease, adult respiratory distress syndrome, allergies,
New human proteases, useful for diagnosis, treatment and prevention of cell proliferative disorders such as atherosclerosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GAGAGITICTIGCICCICTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%; Score 245.4; DB 21; Lengun
99.6%; Pred. No. 1.6e-50;
^ Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 855 BP; 152 A; 283 C; 257 G; 162 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ankylosing spondylitis and amyloidosis.
                                                                                                        Claim 9; Page 105; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS76343 standard; cDNA; 906 BP.
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2000US-0649167
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| 551 GGCTGGA 557
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98US-0065661

W09954343-A2

23-APR-1999; 23-APR-1998;

28-OCT-1999

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RESULT 8
AAD12570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 906;
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99.6%; Pred. No. 1.6e-50;
tive 0; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 12147; 103pp; English.
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246; Conservative
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WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                         P-PSDB; ABG12156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GGCTGGA 247
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                                                                                                                                                                                                                                                            biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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δλ

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This represents the coding sequence of the human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology.
THE T139 cDNA insert is deposited with APCC under accession number.
98684. The T139 polypeptides and polynucleotides can be administered therapeutically or prophylactically to treat/prevent disorders, associated with aberrant T139 expression or activity, especially proliferative or differentiative disorders, e.g. of the immune system. They can be used to differentiative disorders e.g. of the immune system. They can be used to spermatogenesis, e.g. of the immune system. They can be used to spermatogenesis or to treat disorders related to defects in sperm-egg fusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively brinding compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating polypeptide activity. The polyprucleotides are useful for producing probes or primers that conficulating the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant T139 levels; determining if a gene cells or tissues expressing aberrant T139 levels; determining and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate/prevent T139 expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAGITICITGCTCCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCTCTGTGGAATCCCAACCCGGGCTGGGCATCCGGCCTGTGGCGCCACCTGCAAGTG 240
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                                                                                                                                                                                                                                                                                                              Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%; Score 245.4; DB 20; Length 1338; 99.6%; Pred. No. 1.7e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                         (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 114; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246; Conservative
                                                                                                                                                                                                                                                        WPI; 1999-633969/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                               P-PSDB; AAY41266.
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                                                                                                                                                                                                                  Holtzman D;
                                                                                                                                                                                                                                                                                                                                                          activity
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Matches
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The present sequence is human protein with hydrophobic domain encoding count clone HP10760. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides associated with inappropriate polypeptide expression. The polynucleotides into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional culturing the immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate controlling contraction's disease and Alzhaimer's disease), to modulate activin and inhibin activity (e.g. for controlling
                                                                                                                                     Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autofimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Albeimer's disease; chemotratic; chemotric; hamour growth inhibitor; anabolic; chemotraceptive; antiinfertility; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Mature human protein with hydrophobic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
                                                                                                   Human protein having hydrophobic domain encoding cDNA clone HP10760.
                                                                                                                                                                                                                                                                                                                                                                     /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 271-275; 563pp; English.
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
62..1402
AAD12570 standard; cDNA; 1775 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000JP-0000588.
; 2000JP-0005288.
; 2000JP-0002299.
; 2000JP-0026862.
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(SAGA ) SAGAMI CHEM RES CENT
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                                                                        (first entry)
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11-JAN-2000;
03-FEB-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                        25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
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                                    AAD12570;
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fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                            200 GAGAGITICTTGCTCCTCCCTGCACAACCGCCTGCGCAGGTGGGTCCAGCCCCTGCG 259
                                                                                                                                                                                                                                         121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
                                                                                                                                                             140 GAGGTGTGGCCACCCCAGCTGCAGGAGCAGCTCCGATGGCCGGAGCCCTGAACAGGAAG 199
                                                                                                                                                                                      GAGAGITITCITGCICCICCICCTGCACAACCGCCIGCGCAGCIGGGICCAGCCCCTGCG 120
                                                                                                                                  1 GAGGIGIGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG 60
                                                                                                            Gaps
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                                                                                DB 22; Length 1775;
                                                                                                         1; Indels
                                                    Sequence 1775 BP; 360 A; 541 C; 549 G; 325 T; 0 other;
                                                                               Score 245.4; DB 2;
Pred. No. 1.7e-50;
0; Mismatches 1.
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/product= "T139 protein"
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95..1435
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ23299 standard; cDNA; 1856 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human T139 protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 1; 115pp; English.
                                                                                   99.4%;
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                                                                                                Best Local Similarity 99.6
Matches 246; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              380 GGCTGGA 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ23299;
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                                                                                    Query Match
                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ23299
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expressed by standard recombinant methodology. The T139 cDNA insert is deposited with ATCC under accession number 98694. The T139 polypeptides and polynucleotides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant T139 prophylactically to treat/prevent disorders associated with aberrant T139 expression or activity, especially proliferative or differentiative disorders, e.g. of the immune system. They can be used to modulate spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat testicular disorders e.g. testicular cancer. The be useful to treat testicular disorders e.g. testicular cancer. The polypebtides may be used to identify selectively binding compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating probes or primers that selectively hybridize to the compounds confice or produciocides which may be useful for detecting the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant dentify subjects at risk for or having a disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for prevent T139 expression.
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121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
                                                                                                                                                                                                               352
                                                                                                                                                                                                                               181 GCCCTCTGTGGAATCCCCAACCCCGAGCCTGGCCATCCGGCCTGTGGCGCACCCTGCAAGTG 240
                                                                                                                                                                                                                                              1 GAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG 60
                                                         0; Gaps
                                                                                                                             GAGAGTTTCTTGCTCCTCCTCCTGCAACCGCCTGCGCAGCTGGGTCCAGCCCCTGCG
                                                                                                                                                                                            DB 20; Length 1856;
                          99.4%; Score 245.4; DB 20; Length 99.6%; Pred. No. 1.7e-50; 1.ve 0; Mismatches 1; Indels
Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;
                                  Watches 246; Conservative
                                                                                                                                                                                                                                                                                  241 GGCTGGA 247
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                            Query Match
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cytostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilliser; hypotensive; tumour; injury; trauma; antianginal; vasotropic; antiulcer; apoptotic disorder; rheumatoid arthritis; cardiant; renal disorder; hepatotropic; antipsoriatic; antiallergic; dermatological; virucide;
                                                                                                                                                            neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease; heart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive; glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; haemostatic; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic;
                                                                                                                                             Human; haematopoiesis; clotting; kidney failure; wound healing; cancer;
                                                                                             Human T139 (TANGO-139) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; ss.
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Homo sapiens

AAD33531 standard; cDNA; 1856 BP.

AAD33531

01-JUL-2002 (first entry)

AAD33531;

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The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-125), T125 (TANGO-125), T110 (TANGO-110), murine T175 crumurine WDNM-2, having diagnostic, preventive, (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive, the control of the invention has the ability to modulate coll-cell interactions, to inhibit a proteinase activity, to modulate coll-cell interactions, contrologies and thea ability to modulate coll-cell interactions, polynucleotide of the invention are useful for diagnosting and treating disorder characterised by their aberrant expression or activity. The callular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful in wound healing and for treating variety of TANGO-135 is useful in wound healing and for treating cancer, are useful to treat pancreating cancer, are useful to treat pancreating disorders, such as the part disorders, such as useful to treat pancreatic disorders, such as some to the brain. TANGO-125, 110, 175 molecules treat disorders, e.g., creebrowscular disease, and tumours, and injury or trauma (c) the brain. TANGO-139, 125, 110, 175 molecules are useful to treat concertificated diseases and disorders, such as ischaemic heart disease. TANGO-139, 125, 110 and 175 molecules are useful to treat concertions and disorders, such as glomerulonephritis), TANGO-175 is useful to treat of sorders, such as glomerulonephritis), TANGO-175 is useful to treat concert of disorders, such as inflammatory diseases and disorders, inflammatory diseases and summune are useful for treating proliferative disorders, inflammatory diseases and disorders, inflammatory diseases and disorders, inflammatory diseases and summune are also disorders, inflammatory diseases and disorders, inflammatory diseases and disorders, inflammatory diseases and summune are also disorders, inflammatory diseases, remained t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders
                                                                                                                                                               /*tag= c
/product= "Human mature T139 protein"
95..1432
/*tag= d
/note= "This region designated as SEQ.ID.No.3 is specifically referred in claim 27"
                                                                /*tag= a
/product= "Human T139 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodearl ADJ, Mccarthy SA;
                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 26; Fig 1; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0065661.
98US-0102705.
98US-0124538.
                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2001; 2001US-0790264.
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173..1432
                                            .1435
                                                                                                                     /*tag=
                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOLT/) HOLTZMAN D A.
(GOOD/) GOODEARL A D J.
(MCCA/) MCCARTHY S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-303420/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE21077.
                                                                                                                                                                                                                                                                                                   US2002028508-A1.
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                                                                                                                                                                                                  misc_feature
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22-JUN-1998;
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                                                                                                  sig_peptide
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                                                                                                                                          mat_peptide
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(including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and any involving abnormal anglogenesis, neurodegeneration and/or
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                                                                                 infectious diseases.
                                                                                                                                                   Query Match
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AAH98469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding 26 human secreted polypeptides, useful e.g. for preventing, diagnosing and/or treating cancers and for promoting wound
                                                                                                                                                                                                                                                                                                                                    121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                               353 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGGGCTCGGGCCTGTGGGCACCCTGCAAGTG 412
           disorders, cell growth disorders, e.g., cancers and inflammatory disorders and apoptotic disorders. The nucleic acids of the invention are used in gene therapy. The present sequence is human T139 cDNA.
                                                                                                                                                                                                              61 GAGAGITICITGCTCCTCCTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCTGCG 120
                                                                                                                                                                                                                                                                                  233 GAGAGTTCTTGCTCCTCCCTGCACAACCGCCTGCGCAGGTGGGTCCAGCCCCTGGG 292
                                                                                                                                                                                                                                                                                                                                                                          293 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 352
                                                                                                                                                                                         1 GAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG 60
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to 26 secreted human proteins. The proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers
                                                                                                                                                                                                                                                                                                                                                                                                              GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shi Y;
Young PE;
                                                                                                                   99.4%; Score 245.4; DB 24; Length 1856; 99.6%; Pred. No. 1.7e-50;
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                                                                                                                                                         1; Indels
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Florence KA, Ni J,
                                                                                 Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;
                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 416-417; 530pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF24152 standard; DNA; 1923 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duan RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-2000; 2000WO-US15187
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                                                                                                                                                           Matches 246; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061741/07.
                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 GGCTGGA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GGCTGGA 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   healing -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF24152
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                                                                                                                                                                                                                                                                                                       181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG 240
                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                         1 GAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asundi V;
                                        DB 22; Length 1923;
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                                                                                1; Indels
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Sequence 1923 BP; 444 A; 568 C; 569 G; 342 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human EST-derived coding sequence SEQ ID NO: 326.
                                        Score 245.4; DB 27
Pred. No. 1.7e-50;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou P, Qian XB, Wang
A, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH98469 standard; cDNA; 517 BP.
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2001; 2001WO-US02687
                                            99.48;
                                                           Best Local Similarity 99.6%;
Matches 246; Conservative
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P-PSDB; AAM23810.
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458 GGCTGGA 464
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                      proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess blodiversity and for nutritional purposes. The present sequence is a cDNA
            present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                         378
                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                              259 GAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primers useful for synthesizing full length cDNA clones and their
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                         1 GAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAG
                                                                                                                                                                                                                                                                           61 GAGAGTITCTIGCTCCTCCTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCTGCG
                                                                                                                                                                                                                                                                                                                                121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA
                                                                                                                                                                                                                                                                                                                                                                                       181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG
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T, Koga
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0
                                                                                                                                                              98.7%; Score 243.8; DB 22; Length 517; 99.2%; Pred. No. 3.6e-50; Indels 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                    Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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S, Otsuki
                                                                                                                                    Sequence 517 BP; 89 A; 180 C; 159 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s'
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Sugiyama T, Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0194486.
2000JP-0118774.
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                                                                                                                                                            Query Match
Best Local Similarity 99.2'
Matches 245; Conservative
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                                                                                                          of the invention.
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11-JAN-2000;
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Claim 2; SEQ ID NO 290; 1380pp + sequence listing; English

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                 271
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                                                                                                                                                                                                                                                                                                                                                               211
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S, Otsuki T, Koga
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0
                                                                                                                                                                                                                                                            DB 22; Length 512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA clone representative sequence, SEQ ID NO: 1693.
                                                                                                                                                                                                                                                         98.1%; Score 242.2; DB 22; Length
98.8%; Pred. No. 8.8e-50;
Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                         Sequence 512 BP; 94 A; 166 C; 167 G; 82 T; 3 other;
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Sugiyama T, Nagai K, Kojima
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32-MAY-2000; 2000JP-0183765
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Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-524255/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 GGCTGGA 398
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                                                     clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length colors are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAGAGTTTCTTGCTCCTCTTCCCTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         212 GAGAGTTCTTGCTCCTCCTCCCTGCACAACCGCCTGGGCTGGGTCCAGCCCCCTGGG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 GCCCTCTGTGGAACCCCGAACCCCGAGCCTGGCGTCCGCCCGTGGCGCCCTGCAAGTG 391
                                                                                                                                                                                                                                                                                                                                                                            152 GAGGTGTGGCCACCCCAGCTGCAGAGCACCACCATGGCCGGAGCCCTGAACAGGAAG 211
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3, Otsuki T, Koga H;
                                             The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 GCTGACATGCGGAGGCTGGACTGGACTGGCCTCGGCCCAACTGGCTCAAGCCAGGGCA
                                                                                                                                                                                                                                                                                                                              ;
             SEQ ID NO 1693; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                            98.1%; Score 242.2; DB 22; Length 512; 98.8%; Pred. No. 8.8e-50; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                Sequence 512 BP; 94 A; 166 C; 167 G; 82 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota T, Nishikawa T, Isogai T, Hayashi K, IS)
Wakamatsu A, Sugiyama T, Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human full-length cDNA, SEQ ID NO: 2850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK94246 standard; cDNA; 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.88
Matches 244; Conservative
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              Example 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-dends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human cDNA of the invention.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAGITICITGCICCICICCCCGCACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.1%; Score 242.2; DB 22; Length 1786; 98.8%; Pred. No. 1e-49; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                      Claim 8; SEQ ID NO 2850; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1786 BP; 361 A; 548 C; 553 G; 324 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 28, 2002, 17:01:50 Job time : 54.913 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 244; Conservative
WPI; 2001-524255/58.
P-PSDB; AAM93326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GGCTGGA 247
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(without alignments)
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                                                                                                                                                                 December 28, 2002, 20:22:13 ; Search time 70.356 Seconds
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/ Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
/ Ggn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363474 seqs, 203117208 residues
                                                                                                                                                                                                                                                                                       US-09-944-896-49_COPY_123_1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_NA:*
                                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Perfect score:
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Maximum DB :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 49, Appl Sequence 49, Apsequence 3, Apsequence 4, Apsequence 4, Apsequence 4, Apsequence 4, Apsequence 4, Apsequence 4, Apsequenc Sequence 1, Ag Sequence 12, Ag Sequence 12, A Description Seguence US-09-866-018-49 US-09-944-449-49 US-09-944-449-49 US-09-945-587-49 US-09-945-015-49 US-09-944-336-49 US-09-944-432-49 US-09-944-432-49 US-09-944-654-49 US-09-944-654-49 US-09-944-413-49 US-09-944-403-49 US-09-944-896-49 US-09-944-944-49 US-10-042-141-12 US-09-726-643-12 US-09-790-264-3 US-09-790-264-1 SUMMARIES 10 DB Query Match Length 1876 1876 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 94.6 94.6 94.6 100.0 Score 1326 1326 1326 1326 1326 1326 1326 1326 1326 1254 1254 1254 Result 8

88721 88721 5533, 333, 553, 553, 553, 553, 553, 553	75, 221 222 107 7, A
\$0 \$0 \$0 \$0 \$0 \$0 \$0 \$0 \$0 \$0 \$0 \$0 \$0 \$	US-09-764-870-75 US-09-764-870-221 US-09-764-870-222 US-09-833-381-1076 US-10-068-347-7
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ALIGNMENTS

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APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THILE REFERENCE: P2548PIG.
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/944,413
CURRENT APPLICATION NUMBER: US/09/944,413
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: December 3, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
                          Sequence 49, Application US/09944413
Patent No. US20020156004A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       Grimaldi, Christopher
                                                                                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                 Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
                                                                                                          APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Hillan, Kenneth
                                                                                                                                                                     Eaton, Dan
US-09-944-413-49
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APPLICANT:
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APPLICANT:
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1021 AAAGTGCAGGACATCCTGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 1080
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       PRIOR APPLICATION NUMBER: 60/069,702
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR PELICATION NUMBER: 60/069,873
PRIOR PELICATION NUMBER: 60/069,873
PRIOR PELING DATE: December 114, 1997
PRIOR PELING DATE: December 134, 1998
PRIOR FILING DATE: FEDTUATY 9, 1998
PRIOR PELICATION NUMBER: 60/074,086
PRIOR PELICATION NUMBER: 60/074,086
PRIOR PELICATION NUMBER: 60/075,945
PRIOR PELICATION NUMBER: 60/075,945
PRIOR PELICATION NUMBER: 60/075,945
PRIOR PELICATION NUMBER: 60/112,856
PRIOR PELICATION NUMBER: 60/112,856
PRIOR PELICATION NUMBER: 60/112,986
PRIOR PELICATION NUMBER: PCT/US99/1230
PRIOR APPLICATION NUMBER: PCT/US99/1230
PRIOR APPLICATION NUMBER: 90/216,01
PRIOR APPLICATION NUMBER: PCT/US99/1235
PRIOR APPLICATION NUMBER: PCT/US99/1235
PRIOR APPLICATION NUMBER: PCT/US99/12301
PRIOR PELING DATE: NUMBER: PCT/US99/12301
PRIOR APPLICATION NUMBER: PCT/US99/1301
PRIOR PRIOR PLING DATE: MAY 22, 2000
PRIOR PRIOR PLING DATE: MAY 22, 2000
PRIOR PRIOR PLING DATE: MAY 22, 2000
PRIOR PLING APPLICATION NUMBER: PCT/US99/12678
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
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LENGTH: 1876
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1141 TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCCAGCCT 1200
                                                                                                                                   1323 GACAACCACGGGCTGGTGTGCTGCTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG 1382
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                       GACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG
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CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 06/065,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR PELICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR FILING DATE: FEBRUARY 9, 1998
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Roy, Margaret
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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020165143A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020165143A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
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100.0%; Score 1326;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/105,945
PRIOR PELLING DATE: February 25, 1998
PRIOR FILING DATE: PEDCHALL 10,12,1998
PRIOR PELLING DATE: December 16, 1998
PRIOR PELLING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PELLORATION NUMBER: POT/US98/1930
PRIOR PELLORATION NUMBER: POT/US98/1930
PRIOR PELLORATION NUMBER: 09/216,021
PRIOR PELLORATION NUMBER: 09/216,021
PRIOR PELLING DATE: December 16, 1998
PRIOR PELLORATION NUMBER: 09/218,517
PRIOR PELLING DATE: December 16, 1999
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PRIOR PELLING DATE: PERTON SOURCE 1999
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PRIOR PELLING DATE: December 16, 1999
PRIOR PELLING DATE: PETURS POT/US09/28313
PRIOR PELLING DATE: PETURS POT/US09/0414
PRIOR PELLING DATE: PEDCHARY 22, 2000
PRIOR PELLING DATE: FEBRUARY 22, 2000
PRIOR PELLING DATE: FEBRUARY 22, 2000
PRIOR PELLING DATE: PEDCHARY 22, 2000
PRIOR PELLING DATE: MAY 22, 2000
PRIOR PELLING DATE: PEDCHARY 28, 2001
PRIOR PELLING DATE: PEDCHARY 28, 2001
PRIOR PELLING DATE: PEDCHARY 28, 2001
PRIOR PELLING DATE: PEDCHARY 2007
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            CTGGCTCAAGCCAGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG
                                                       TGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCCTTT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: D0-05-25
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: D0-05-25
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: D0-05-31
PRIOR PRILING DATE: D0-05-31
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DR APPLICATION NUMBER: 60/075,945
DR FILING DATE: February 25, 1998
DR APPLICATION NUMBER: 60/112,850
DR FILING DATE: December 16, 1998
DR APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
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                                                                                                                                                                             Sequence 49, Application US/09944896 Patent No. US20020168715A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski,Paul
Grimaldi,Christopher
                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara, Napoleone
Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Kevin APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary
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Tumas, Daniel
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kljavin, Ivar
Napier, Mary
                                                                                                                                                                                                                                                                                                                                                                       Eaton, Dan
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1443 TGCCAG 1448
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543 TGTGCTCGCAACGCCACCTGCACCTACACGCAGCTCGTGTGGGGCCACCTCAAGCCAG
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APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR PILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. US20020168715Alember 30, 1999
PRIOR FILING DATE: POT/US99/28301
PRIOR FILING DATE: POT/US99/28301
PRIOR FILING DATE: PEDUARY 11, 2000
PRIOR FILING DATE: FEDUARY 11, 2000
PRIOR FILING DATE: FEDUARY 22, 2000
PRIOR FILING DATE: FEDUARY 22, 2000
PRIOR FILING DATE: MATCH 3, 2000
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PRIOR PLING DATE: PEDUARY 24, 2001
PRIOR PLING DATE: PEDUARY 28, 2001
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LENGTH: 1876
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                  GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILING DATE: No. US20020173463Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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BR FILING DATE: December 22, 1998

PRELING DATE: December 20, 1998

PRELING DATE: July 28, 1999

BR APPLICATION NUMBER: PCT/MC98/19330

BR APPLICATION NUMBER: PCT/MC98/1938

BR APPLICATION NUMBER: PCT/MC98/25108
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CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/0S99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/0S99/21090
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APPLICATION NUMBER: PCT/US99/28409
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 00/669,334
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PRIOR DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069,278
PRIOR PELICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 12, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: Pebruary 9, 1998
PRIOR PELING DATE: Pebruary 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: February 9, 1998
PRIOR PELING DATE: Pebruary 9, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: PELIN
                                                         Godowski, Paul
Grimaldi, Christopher
                                                                                                                  Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Gerritsen, Mary
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Tumas, Daniel
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243 GGAGCCCTGAACAGGAAGGAGAGTTTCTTGCTCTCCCTGCACAACCGCCTGCGAGC 302
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100.0%; Pred. No. 0;
iive 0; Mismatches
        PRIOR FILING DATE: DECEMBLI, 199
PRIOR PELICATION NUMBER: PCT/0599/30095
PRIOR FILING DATE: DECEMBER 16, 1999
PRIOR FILING DATE: PEDRUARY 11, 2000
PRIOR FILING DATE: FEBRUARY 12, 2000
PRIOR FILING DATE: FEBRUARY 22, 2000
PRIOR PELICATION NUMBER: PCT/0500/04414
PRIOR APPLICATION NUMBER: PCT/0500/05841
PRIOR PILING DATE: MATCH 2, 2000
PRIOR PILING DATE: MATCH 2, 2000
PRIOR FILING DATE: MATCH 30, 2000
PRIOR FILING DATE: MATCH 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: DATE APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: DECEMBER 1, 2000
PRIOR FILING DATE: PEDRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
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ORGANISM: Homo Sapien
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1081 GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC 1140
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GCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA 720
         781 CAAGTGAGGTGCAGCCTGCAGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGGTCGTGC 840
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                                           721 CGTCTCAACATCAGCACCTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC
                                                                                                     901 ACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTTTCAGAGGCAGACACCTAT
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Patent No. US20020058309A1
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Grimaldi, Christopher
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Filvaroff, Ellen
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Napier,Mary
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                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult Palm or file wrapper
NUMBER OF SEQ ID NOS: 120
                                                                                                                                                                    0; Indels
                                                                                                                                       100.0%; Score 1326; I
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                              Matches 1326; Conservative
                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
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                                                                                                              US-09-866-028-49
                                                               SEQ ID NO 49
                                                                                                                                        Query Match
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020102647Alember 30, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: Pebruary 9, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR PLING DATE: Pebruary 26, 1998
PRIOR PLING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PLING DATE: December 16, 1998
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PRIOR APPLICATION NUMBER: CT/US98/1930
PRIOR PLING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: O9/216,021
PRIOR PLING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
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PRIOR FILING DATE: MATCH 3, 1999
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PRIOR FILING DATE: SEPTEMBER: CT/US99/21090
PRIOR FILING DATE: SEPTEMBER 15, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: PEDTUARY 22, 2000
PRIOR FILING DATE: PEDTUARY 22, 2000
PRIOR FILING DATE: MATCH 2, 2000
PRIOR PRIOR DATE: MATCH 2, 2000
PRIOR PILING DATE: MATCH 2, 2000
PRIOR PRILING DATE: MATCH 2, 2000
PRIOR PILING DATE: MATCH 3, 2000
PRIOR PILING DATE: MATCH 3,
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                                PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 18, 1997
PRIOR FILING DATE: ADMINISTRES 60/070,440
PRIOR PRIOR APPLICATION NUMBER: 60/070,440
                                                                                                                                                                                                                                                                           APPLICATION UNDBER: 60/668,017
FILING DATE: December 18, 1997
APPLICATION NIMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
APPLICATION NUMBER: 60/069,696
                             FILING DATE: December 16, 1997 APPLICATION NUMBER: 60/069,694
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US-09-944-449-49
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Best Local Similarity
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LENGTH: 1876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1323 GACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG 1382
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                                                                                                             1023 ACCTGTGACCTGAGGATCGACGGAGAGCTGCTTCATGGTGTCTTCAGAGGCAGACACATAT 1082
                                                                                                                                                                                                 961 TACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
                                                                                                                                                                                                                           1083 TACAGAGCCAGGATGAAATGTCAGAGGAGAGGGGGGTGCTGGCCAGATCAAGAGCCAG 1142
                                                                                                                                                                                                                                                                                                                        1021 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 1080
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                                                                          901 ACCIGIGACCIGAGGATCGACGGAGACTGCTICAIGGIGTCTICAGAGGCAGACACCTAI 960
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APPLICATION NUMBER: 60/069,425
FILING DATE: December 12, 1997
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Patent No. US20020102647A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Hillan, Kenneth
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961 TACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
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         TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGAGTGACAGCCTGGCCCAA
                                                                                CTGGCTCAAGCCAGGCCACCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG
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       PRIOR FILING DATE: January 5, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR PELICATION NUMBER: 60/074,092
PRIOR PELING DATE: FEBRUARY 9, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR PELING DATE: FEBRUARY 25, 1998
PRIOR PELING DATE: FEBRUARY 25, 1998
PRIOR PELING DATE: PEBRUARY 25, 1998
PRIOR PELING DATE: DECEMBER: 60/146,222
PRIOR FILING DATE: DECEMBER: 60/146,222
PRIOR PELICATION NUMBER: 60/146,222
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PRIOR PELING DATE: MARCH 3 1999
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PRIOR PELING DATE: DECEMBER 11, 1999
PRIOR PELING DATE: DECEMBER 11, 1999
PRIOR PELING DATE: DECEMBER 11, 1999
PRIOR PELING DATE: PEBRUARY 11, 2000
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FILING DATE: January 5, 1998
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APPLICANT: TUTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILTE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILTE OF INVENTION: ACIDS ENCODING THE SAME FILTE OF INVENTION: ACIDS ENCODING THE SAME FILTE OF INVENTION: ACIDS ENCODING THE SAME CURRENT PAPLLCATION NUMBER: 09/86,028 PRIOR PLILIAG DATE: 2001-09-26 PRIOR PLILIAG DATE: 2001-05-26 PRIOR PLILIAG DATE: December 3, 1997 PRIOR APPLICATION NUMBER: 09/66,7411 PRIOR APPLICATION NUMBER: 60/66,334 PRIOR PLILIAG DATE: December 11, 1997 PRIOR PLILIAG DATE: December 12, 1997 PRIOR PLILIAG DATE: December 16, 1997 PRIOR PLILIAG DATE: December 17, 1997 PRIOR PLILIAG DATE: Pedender 17, 1998 PRIOR PLILIAG DATE: Pedender 15, 1998 PRIOR PLILIAG DATE: PEDENDER 
1261 CAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACGGTTACATC 1320
                          1383 CAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACATC 1442
                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/09945587 Patent No. US20020127643A1 GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICATION NUMBER: PCT/US99/228409
FILING DATE: NO. US20020127643Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020127643Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
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                                                                             PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: JOHNE 22, 1999
PRIOR FILING DATE: JOHNE 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
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PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PECTYUS99/28313
PRIOR FILING DATE: PECEMBER: PCTYUS99/28301
PRIOR FILING DATE: PECEMBER: PCTYUS99/2809
PRIOR FILING DATE: PECEMBER: PCTYUS99/2809
PRIOR FILING DATE: FEBRUARY 11, 2000
PRIOR APPLICATION NUMBER: PCTYUS00/03465
PRIOR APPLICATION NUMBER: PCTYUS00/0841
PRIOR FILING DATE: FEBRUARY 11, 2000
PRIOR FILING DATE: FEBRUARY 22, 2000
PRIOR FILING DATE: MARCH 2, 2000
PRIOR APPLICATION NUMBER: PCTYUS00/14042
PRIOR FILING DATE: MARCH 2, 2000
PRIOR FILING DATE: MARCH 2, 2000
PRIOR FILING DATE: MARCH 28, 2000
PRIOR FILING DATE: DECEMBER: PCTYUS00/20710
PRIOR APPLICATION NUMBER: 
APPLICATION NUMBER: PCT/US98/19330 FILING DATE: September 16, 1998 APPLICATION NUMBER: PCT/US98/25108
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SEQ ID NO 49
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Best Local Similarity
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ORGANISM: Homo Sapien
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APPLICANY: WOOD, WILLIAM

APPLICANY: WOOD, WILLIAM

TITLE OF INVENTION: SECRETED AND TRANSMERRANE POLYPEPTIDES AND NUCLEIC

FILE REPERENCE: PS548FD. ACIDS SECONDRG THE SAME

FILE SECRETED SECONDRG THE SAME

FRICK PILLIAM DATE: 2001-09-26

FRICK PILLIAM DATE: DOUG-09-26

FRICK FILLIAM DATE: FEDINGER: 00-713-29

FRICK FILLIAM DATE: FEDINGER: 00-713-29

FRICK FILLIAM DATE: DOUG-09-26

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APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                          Godowski, Paul
Grimaldi, Christopher
                                                                                                                      Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napler, Mary
Koy, Margaret
Tumas, Daniel
Wood, William
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
                                                                                                                                                                                Gerritsen, Mary
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   DR FILING DATE: September 15, 1999
DR APPLICATION NUMBER: PCT/US99/28409
DR FILING DATE: No. US20020132768Alember 30, 15
DR APLICATION NUMBER: PCT/US99/28313
DR FILING DATE: No. US2002013278Alember 30, 15
DR FILING DATE: December1, 1999
DR FILING DATE: December1, 1999
DR FILING DATE: December 16, 1999
DR FILING DATE: December 16, 1999
DR PILING DATE: DECEMBER: PCT/US99/30095
DR FILING DATE: DECEMBER: PCT/US90/03565
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100.0%; Score 1326;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR PLILING DATE: NO. US2002013276841ember
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PRIOR PLILING DATE: NO. US2002013376841ember
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLILING DATE: December 16, 1999
PRIOR PLILING DATE: December 16, 1999
PRIOR PLILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PLILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0841
PRIOR PLILING DATE: MAICH 2, 2000
PRIOR PPLICATION NUMBER: PCT/US00/08439
PRIOR PLILING DATE: MAICH 20, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PLILING DATE: MAICH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PLILING DATE: MAICH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/120710
PRIOR PLILING DATE: JULY 28, 2000
PRIOR PLILING DATE: DECEMBER 1, 2000
PRIOR PLILING DATE: DECEMBER 1, 2000
PRIOR PLILING DATE: DECEMBER 1, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR PLILING DATE: FEBRUARY 28, 2001
PRIOR PLILING DATE: FEBRUARY 28, 2001
PRIOR PLILING DATE: FEBRUARY 28, 2001
PRIOR RELING DATE: FEBRUARY 28, 2001
PRIOR PLILING DATE: FEBRUARY 28, 2001
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US-09-945-015-49
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Patent No. US20020132981A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
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Filvaroff, Ellen
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Goddard, Audrey
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APPLICATIVE WOOD MILITIAN AND TRANSMEMBRANE POLIPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFORMY.

THE BETTERMENT OF SECRETED AND TRANSMEMBRANE POLIPEPTIDES AND NUCLEIC CHIRERY APPLICATION NUMBER: 105/02/95/14/396

PRIOR APPLICATION NUMBER: 105/02/95/14/396

PRIOR APPLICATION NUMBER: 60/067/31

PRIOR APPLICATION NUMBER: 60/069/34

PRIOR PILING DATE: December 1/3/397

PRIOR PAPLICATION NUMBER: 60/06/3/397

PRIOR PILING DATE: December 1/3/397

PRIOR PAPLICATION NUMBER: 60/06/3/398

PRIOR PAPLICATION NUMBER: 60/06/3/398

PRIOR PAPLICATION NUMBER: 60/06/3/398

PRIOR PAPLICATION NUMBER: 60/06/3/398

PRIOR PAPLICATION NUMBER: 60/06/3/330

PRIOR PAPLICATION NUMBER: 60/07/3/398

PRIOR PAPLICATION NUMBER: 60/07/3/399

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                                                      Tumas, Daniel
Wood, William
                                                      APPLICANT:
APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR PLICATION NUMBER: PCT/US00/20710
PRIOR PLICATION NUMBER: PCT/US00/20710
PRIOR PLILNG DATE: JULY 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
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PRIOR FILING DATE: FEDURALIA 28, 2001
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Best Local Similarity
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APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Hilan, Kenneth
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P254@PIC1
                                                                                                                                                                                           ACCTGTGACCTGAGGATGGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTAT 960
843 CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC 902
                                    781 CAAGTGAGGTGCAGCCTGCAGTGTGTGTGCACGCCGGTTCCGGGAGGAGGAGGAGTGCTCGTGC
                                                           GTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 13, 1997
PRIOR FILING DATE: DECEMBER 14, 1997
PRIOR FILING DATE: DATE: DECEMBER 14, 1997
PRIOR FILING DATE: DECEMBER 15, 2001
PRIOR FILING DATE: DECEMBER 17, 2000
PRIOR FILING DATE: DECEMBER 17, 2000
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Kljavin, Ivar
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                                          Length 1876;
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                                       100.0%; Score 1326;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                       Query Match 100.
Best Local Similarity 100.
Matches 1326; Conservative
           Homo Sapien
; TYPE: DNA
; ORGANISM: HON
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APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                       GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR PELING DATE: 2001-06-25
PRIOR PELING DATE: December 3, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
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Gurney, Austin
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Godowski, Paul
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020142419ALember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020144419ALember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/075,945
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR PRILOR APPLICATION NUMBER: 60/146,222
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: JULY 28, 1999
PRIOR PELING DATE: JULY 28, 1999
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1999
PRIOR PELING DATE: September 17, 1999
PRIOR PELING DATE: September 16, 1999
PRIOR PELING DATE: September 16, 1999
PRIOR PELING DATE: December 17, 1999
PRIOR PELING DATE: PEPLUARY 11, 2000
PRIOR PELING DATE: MARCH 3, 2000
PRIOR PELING DATE: PEPLUARY 28, 2000
PRIOR PELING DATE: PEPLUARY 28, 2000
PRIOR PELING DATE: PEPLUARY 28, 2001
PRIOR PELING DATE: PEPLUARY 28, 2001
PRIOR PELING DATE: PEPLUARY 28, 2001
                                                                          PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR PRICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
FILING DATE: December 17, 1997
                                                               APPLICATION NUMBER: 60/068,017
                      APPLICATION NUMBER: 60/069,87
                                             DATE: December 17
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US-09-944-432-49
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121 GGAGCCCTGAACAGGAAGGAGATTTCTTGCTCCTCCCTGCACAACCGCCTGCGCAGC 180
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                                                                                                                                                                      303 TGGGTCCAGCCCCTGCGGCTGAATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA 362
                                                                                                                                                                                                          241 CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG 300
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61 CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGCCTCCGATGGCC 120

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1263 TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCT 1322
                                                               1201 GACAACCACGGGCTGGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG 1260
                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT PAPLICATION NUMBER: US/09/943,762
CURRENT FILING DATE: 2001-09-26
PRIOR PAPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: DECEMBER 3, 1997
PRIOR PILING DATE: DECEMBER 1, 1997
PRIOR PILING DATE: DECEMBER 11, 1997
PRIOR PILING DATE: DECEMBER 12, 1997
PRIOR PILING DATE: DECEMBER 16, 1997
PRIOR FILING DATE: DECEMBER 16, 1997
PRIOR FILING DATE: DECEMBER 16, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
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R PAPLICATION NUMBER: 60,074,086
R FILING DATE: FEDERARY 9, 1998
R APPLICATION NUMBER: 60,074,092
R FILING DATE: FEDRUARY 9, 1998
R APPLICATION NUMBER: 60,075,945
R FILING DATE: FEDRUARY 25,1998
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Patent No. US20020142958A1
GENERAL INFORMATION:
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Grimaldi,Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
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APPLICANT: Botstein, David
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                                      PRIOR PELICATION NUMBER: bo(146,222)
PRIOR APPLICATION NUMBER: bo(146,222)
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: JULY 28, 1999
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1999
PRIOR FILING DATE: December 22, 1999
PRIOR FILING DATE: December 15, 1999
PRIOR FILING DATE: December 15, 1999
PRIOR PILING DATE: DECEMBER: POT/US99/12090
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: NO. US20020142958Alember 30, 1999
PRIOR PILING DATE: POT/US99/28301
PRIOR PILING DATE: POCUMBER: POT/US99/28301
PRIOR PILING DATE: POCUMBER: POT/US99/28301
PRIOR PILING DATE: PEDLUARY 11, 2000
PRIOR PELING DATE: PEDLUARY 11, 2000
PRIOR PELING DATE: PEDLUARY 11, 2000
PRIOR PELING DATE: PEDLUARY 30, 2000
PRIOR PELING DATE: PEDLUARY 30, 2000
PRIOR PELING DATE: PRIOR POT/US00/08419
PRIOR PILING DATE: PEDLUARY 30, 2000
PRIOR PELING DATE: PEDLUARY 30, 2000
PRIOR PILING DATE: PEDLUARY 30, 2000
PRIOR PELING DATE: PRIOR NUMBER: POT/US00/08419
PRIOR PILING DATE: PRIOR POT/US00/08419
PRIOR PILING DATE: PAT/US00/08419
PRIOR PILING DATE: PAT/US00/080/08019
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PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
FILING DATE: December 16, 1998 APPLICATION NUMBER: 60/113,296
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CORGANISM: Homo Sapien
US-09-943-762-49
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363 CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG 422

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961 TACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
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                                     361 GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAG 420
                                               TGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGGGGCCACCTCAAGCCAG 480
                                                                                                                        541 GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG 600
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APPLICANT: WOOD William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/944,654
CURRENT FILING DATE: 2001-09-26
CURRENT FILING DATE: 2001-09-26
PRIOR PELING DATE: 2001-05-25
PRIOR PELING DATE: 2001-05-25
PRIOR PELING DATE: DOC-MDEATI, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 12, 1997
PRIOR FILING DATE: DECEMBER 16, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 16, 1997
PRIOR FILING DATE: DECEMBER 16, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 16, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 18, 1999
PRIOR FILING DATE: DECEMBER 18, 1999
PRIOR FILING DATE: EBLUARY 9, 1998
PRIOR FILING DATE: FEBLUARY 9, 1998
PRIOR FILING DATE: DECEMBER 16, 1997
PRIOR APPLICATION NUMBER: 60/0146, 222
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: SEPLUARY 9, 1999
PRIOR FILING DATE: SEPLUARY 9, 1999
PRIOR APPLICATION NUMBER: PCT/US98/1930
                                                        Sequence 49, Application US/09944654
Patent No. US20020142959A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
                                                                                                                                                                                                                                                                                                                                                                        Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
                                                                                                                                                                                                                                  Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                 Baker, Kevin
Botstein, David
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RESULT 14
US-09-944-654-49
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APPLICANT:
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Eaton, Dan
Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: Warch 3, 1999
PRIOR FILING DATE: Warch 3, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020142959Alember 30, 1999
PRIOR FILING DATE: DOCUMER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR PRILING DATE: December 16, 1999
PRIOR PRILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PRILING DATE: PEDTUARY 11, 2000
PRIOR PRILING DATE: FEBTUARY 11, 2000
PRIOR PRILING DATE: FEBTUARY 22, 2000
PRIOR PRILING DATE: FEBTUARY 22, 2000
PRIOR PRILING DATE: FEBTUARY 22, 2000
PRIOR PRILING DATE: MATCH 3, 2000
PRIOR PRILING DATE: MATCH 30, 2000
PRIOR PLILING DATE: JULY 28, 2000
PRIOR PLILING DATE: DECEMBER: PCT/US00/32678
PRIOR PLILING DATE: JULY 28, 2001
PRIOR PLILING DATE: PEDTUARY 28, 2001
PRIOR PLILING DATE: PEDTUARY 28, 2001
PRIOR FILING DATE: PEDTUARY 28, 2001
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100.0%; Pred. No. 0;
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Matches 1326; Conservative
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020150976Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020150976Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/943,851A
CURRENT FILING DATE: 2001-08-30
PRIOR PAPLICATION NUMBER: US/09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: DECEMBER: 60,069,335
PRIOR APPLICATION NUMBER: 60,069,335
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R APPLICATION UNUBER: 09/218,517
R APPLICATION NUMBER: 09/254,311
R FILING DATE: March 3, 1999
R FILING DATE: Warch 3, 1999
R FILING DATE: UNUBER: PCT/US99/12252
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FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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PTI.ING DATE: September 15, 1999
PTI.ING DATE: September 15, 1999
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PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PRICIATION NUMBER: 60/069, 694
PRIOR PILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
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APPLICATION NUMBER: 60/069,870
FILING DATE: December 17, 1997
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FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/075,945
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
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APPLICATION NUMBER: 60/112,850
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
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Grimaldi, Christopher
                                                                                                 Gurney, Austin
Hillan, Kenneth
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Tumas, Daniel
Wood, William
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tive 0; Mismatches
              PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: Pebruary 11, 2000
PRIOR PILING DATE: Pebruary 22, 2000
PRIOR PELICATION NUMBER: PCT/US60/04414
PRIOR PELICATION NUMBER: PCT/US60/04414
PRIOR PELICATION NUMBER: PCT/US60/08419
PRIOR PELICATION NUMBER: PCT/US60/08419
PRIOR PLILING DATE: March 2, 2000
PRIOR PLILING DATE: March 30, 2000
PRIOR PLILING DATE: May 22, 2000
PRIOR PLILING DATE: May 22, 2000
PRIOR PLILING DATE: May 22, 2000
PRIOR PLILING DATE: JULY 28, 2000
PRIOR PLILING DATE: JULY 28, 2000
PRIOR PLILING DATE: JULY 28, 2000
PRIOR PLILING DATE: December 1, 2000
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PRIOR APPLICATION NUMBER: PCT/US99/30095
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         ACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTAT
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-199-87-2
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US-08-125-468-1
US-09-125-468-1
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US-09-125-468-1
US-09-125-468-1
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US-08-445-247-3
US-08-232-015-2
US-08-998-416-567-3
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Sequence 3, Appli
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Sequence 343,
                                      Sequence 7,
Sequence 6,
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
US-08-459-595A-6
US-08-459-504B-6
US-08-459-444-6
US-09-053-549-7
US-09-547-422-6
US-08-923-137-2
US-08-923-137-2
US-08-923-137-2
US-08-914-549A-1
US-08-951-843A-224
US-08-951-843A-224
US-08-951-843A-1
US-08-951-843A-1
US-08-851-843A-1
US-08-851-843A-1
US-08-851-843A-1
US-08-851-843A-1
US-09-675-321-1
US-09-675-321-1
US-09-675-321-1
US-09-675-321-1
                                                                                                                                                                                                                         US-08-974-549A-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURTENDY APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 31/4 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,749
3R: PF-0186 US
                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08773368
; Patent No. 5856130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78; Conservative
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  3624
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
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IMMEDIATE SOURCE:
CLONE: 1599164
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                                                                                                                                                                                                                                                                                                      RESULT 1
US-08-773-368-2
                                                                                          STATE:
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43 GGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCCTCCTGCACAACCGCCTGCGAGC 102
                      103 TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCCAA 162
                                                                                        43 GGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCCCTGCACAACCGCCTGCGAGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGACTGACAGCCTGGCCCAA 162
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                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FSASLEDO for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/199,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy RJ
RECISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0186 US
TELECOMNUNICATION INFORMATION:
TELECHONE: 415-845-4166
                                                                                                                                                         207 TTCGCCAAGGCTACGCACGCAGTNTCG 235
                                                                                                                                    163 CTGGCTCAAGCCAGGGCAGCCCTCTGTGG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/773,368
FILING DATE:
                                                                                                                                                                                                                                                        Sequence 2, Application US/09199887 Patent No. 6071874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
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CITY: Palo Alto
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IMMEDIATE SOURCE:
CLONE: 1599164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 GGAGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCTT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Fatent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
TITLE OF INVENTION DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Indels
                                                                                                                                                                                      PATCHL NO. 0203202
APPLICANT: Sherman, D.H.
APPLICANT: Sherman, D.H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, I.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438021
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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13.7%; Score 33.8; Dr
Best Local Similarity 54.4%; Pred. No. 4.6;
Matches 68; Conservative 0; Mismatches
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                         207 TTCGCCAAGGCCTACGCACGCAGTNTCG 235
163 CTGGCTCAAGCCAGGGCAGCCCTCTGTGG 191
                                                                                                                                                      Sequence 30, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-5
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LENGTH: 13842
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                                                                                                          RESULT 3
US-09-105-537-30
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US-09-105-537-5
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Matches
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5089 GCCTGCCGCTGCCCGGTGGGGTCGCCTGCCGGAGCTGTGGCGGCTGGCGGG 5148
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                                                                                                                                                                                                                                                                                                                                                   APPLICANI: TANO, LI

TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT PILING DATE: 1999-05-27
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER PILING DATE: 1998-06-26
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-08
EARLIER FILING DATE: 1998-05-08
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
CONTRACT OF SEQ ID NOS: 34
CONTRACT OF SEQ ID NOS: 34
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APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Gaffney, Thomas D.
APPLICANT: Torkewitz, Nancy
TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
TITLE OF INVENTION: with Enhanced Biocontrol Activity
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.7%; Score 33.8; DB 3; Length 38506; nilarity 54.4%; Pred. No. 5.5; Conservative 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Indels
                                                                                                                                                                                                            Sequence 19, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-761-258-8; Sequence 8, Application US/08761258; Patent No. 5756087
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, MARY C.
APPLICANT: MCDANIEL, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                       5149 CGGCG 5153
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                                                               144 GAGTG 148
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US-09-320-878-19
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Matches
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82 CIGCACAACCGCCIGCGCAGCIGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGAC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "potential ribosome binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

LOCATION: 256.3006
OTHER INFORMATION: /product= "LemA"

CTHER INFORMATION: /note= "LemA coding sequence."
                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/761,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Pseudomonas fluorescens
CGA267356 (aka MOCG134 and aka BL915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.2%; Score 32.6; DB 1; 52.6%; Pred. No. 7.3; Live 0; Mismatches 64;
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Me192, J. TIMOCHY
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEFHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08977306
Patent No. S955348
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Gaffney, Thomas D.
APPLICANT: Torkewitz, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 245..251
OTHER INFORMATION: /note
OTHER INFORMATION: site"
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3186 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1042 ACCATCGAGATCCAG 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Conservative
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                                                                                                                  COMPUTER READABLE FORM:
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LOCATION: 245..251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
          STREET: 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                              10591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                    CITY: Ta.
STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 CTGCACAACCGCCTGCGCAGCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGAC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
TITLE OF INVENTION: Genetically Modified Pseudomonas Strains TITLE OF INVENTION: with Enhanced Biocontrol Activity NUMBER OF SEQUENCES: 11
ADDRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Indels
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.2%; Score 32.6; DB 2;
Best Local Similarity 52.6%; Pred. No. 7.3;
Matches 71; Conservative 0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356 (aka MOCG134 and aka BL915)
                                                                        AUDKESSEE: No. 5955348artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: NC
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/977,306 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3186 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; Patent No. 6048702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: site
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                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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LOCATION: 245..251
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
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FEATURE:
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APPLICANT: Prendergast, George C. APPLICANT: Sakamiro, Daltoku APPLICANT: Sakamiro, Marine and Human Box-Dependent TITLE OF INVENTION: MYC-Interacting Protein (Bin1) and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 CAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCTCCCTGCAC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 GACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.1%; Score 32.4; DB 3; Length 2808; Best Local Similarity 46.4%; Pred. No. 8; Matches 102; Conservative 0; Mismatches 118; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 2211..2213
; OTHER INFORMATION: /note= "start site for translation; OTHER INFORMATION: initiation"
US-08-870-126-7
                                                                                                                                    ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr,, P O Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2629 caaggeccnggaagcirggaagccagriggigaccicna 2668
                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: POCT-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/870,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CIGGCATCCGGCCTGTGGCGCACCCTGCAAGTGGGCTGGA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,972
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST60CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 2051..2294
OTHER INFORMATION: /note= "exon 1"
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERFATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2808 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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2211..2213
                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson an
                                                                                                                                                                                                                            Pennsylvania
                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 GACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 CAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCCTGCAC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 2211..2213
OTHER INFORMATION: /note= "start site for translation initiation"
                                                                                                                          Prendergast, George C. Sakamuro, Daitoku
TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
(Bin1) Compositions and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 32.4; DB 4; Length 2808; 46.4%; Pred. No. 8; tive 0; Mismatches 118; Indels 0;
                                                                                                                                                                                                                                                                           STREET: Spring House Corporate Cntr, P O Box 457 CITY: Spring House STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                     APPLICANT: Wistar Institute of Anatomy & Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/445,247
FILING DATE: 03-Dec-1999
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/870,126
FILING DATE: 06-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 2051..2294
OTHER INFORMATION: /note= "exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: WST6ODPCT TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEPAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                           ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                        Sequence 7, Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2808 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPOLOGY: unknown
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Matches 102; Conservative
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
               US-09-445-247-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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RESULT 9
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Cloning of the biosynthetic pathway for chlortetracycline and tetracyline Formation and cosmids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17577 CCTTCTCGCACTACCGGTGTGGAACTCGGTCTTCCGGATCTGGGCCTCGGCCAGCGTGA 17636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 32.4; DB 1; Length 30001; 46.8%; Pred. No. 12; tive 0; Mismatches 116; Indels 0;
                         2629 CAAGGGCCNGGAAGCTTGGGAAGCCAGTTGGTGACCTCNA 2668
208 CTGGCATCCGGCCTGTGGCGCACCTGCAAGTGGGCTGGA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17697 ACTGCCAGGCGCTGGACGACAACCCGTACCCGGGCCTG 17734
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                                                                                                                                                                                                                                                                                                                                                                                     American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/125,468 FILING DATE: 22-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                            useful therein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         Sequence 1, Application US/08125468
Patent No. 5589385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: TSevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                                                                                                                                                                          APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning
TITLE OF INVENTION: chlortet
TITLE OF INVENTION: useful F.
                                                                                                                                                                                                                                                                                                                                                                                                      One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                  APPLICANT: Ryan, Michael J. APPLICANT: Lotvin, Jason A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : (201)831-3241
(201)831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                         Wayne
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                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                              RESULT 10
US-08-125-468-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-125-468-1
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US-08-474-933-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation and cosmids
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.1%; Score 32.4; DB 2; Length 30 Best Local Similarity 46.8%; Pred. No. 12; Matches 102; Conservative 0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 17697 ACTGCCAGGCGCTGGACGACAACCCGTACCCGGGCCTG 17734
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentII Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/474,933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 CAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION

NAME: TSEVEDIE 31,145

REGISTRATION NUMBER: 31,145

REFERENCE/DOCKET NUMBER: 31,25

TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-324

INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
Sequence 1, Application US/08474933
Patent No. 5866410
                                                                                                                                                                                                                                                                                         One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                        New Jersey
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                                                                                                                                                                                                                                                                                                                 Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-474-933-1
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ISOLATION OF THE BIOSYNTHESIS GENES FOR PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS GLA.O AND THEIR USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.0%; Score 32.2; DB 4; Length 465;
Best Local Similarity 50.3%; Pred. No. 6.7;
Matches 79; Conservative 0; Mismatches 78; Indels
APPLICANT: Lodes, Michael J.
APPLICANT: Acarist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
TITLE DE INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210.121.47501
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
BARLIER APPLICATION NUMBER: US 09/285,323
EARLIER APPLICATION NUMBER: US 09/285,323
SAFINER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE FASTSEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NAMER: US/09/194,905 FILING DATE: 29-JUL-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 TGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 TCATCATACTGCAAGTTTGCCACAACCTCCTGCATCT 183
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APPLICATION NUMBER: WO PCT/EP97/02826

FILING DATE: 30-MAY 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 19622783.6

FILING DATE: 07-JUN 1996

ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33.683
REFERENCE/DOCKET NUMBER: 026083/0193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: Patentin Pales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09194905
Patent No. 6306627
GENERAL INFORMATION:
APPLICANT: DECKER, Heinrich
TITLE OF INVENTION: PSEUDO-OLIGOS?
TITLE OF INVENTION: GLA.O AND THEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: FOLEY & I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapien US-09-370-838-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3000 K SI
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-194-905-7/c
                                                                                                                                                                                                                                                                                                               SEQ ID NO 229
LENGTH: 465
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                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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                 HYPOTHETICAL:
                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                96 GCGCAGCTGGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGACAGCCT 155
                                                                                                                                                                                                                                                                                                                                                                                                 957 GCTCGGCCAGGTACGCGCCTCGGACTGCTGGGGCCTGGAGTTCGTCACCGACGCGT 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 GCCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATC 215
                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                    36 GATGGCCGGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCCTCCACACCGCCT 95
                                                                                                                                                                                                          Query Match
13.0%; Score 32.2; DB 4; Length 6854;
Best Local Similarity 47.7%; Pred. No. 11;
Matches 94; Conservative 0; Mismatches 103; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Katz, L
APPLICANT: Katz, L
APPLICANT: Nacalpine, S
APPLICANT: Macalpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: ETYTHRONGIN Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
CARDESSEE: Edward H: Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Abbott Laboratories D377/AP6D-2 One Abbott STREET: Park Rd CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/07642734C Patent No. 5824513 GENERAL INFORMATION:
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6854 base pairs
TYPE: nucleic acid
STRADENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4955
TELECOMMUICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-194-905-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 20235 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 CGGCCTGTGGCGCACCC 232
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SATURE:
NAME/KEY: CDS
LOCATION: 19..10722
OTHER INFORMATION: /codon_start= 19
OTHER INFORMATION: /function= "gene erya"
OTHER INFORMATION: /function= "gene erya"
OTHER INFORMATION: /product= "erya ORF2 encoding modules 3 & 4 for "anamion: 6-deoxyerythronolide B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 4471..5847
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and encylreductase domains m"
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 97.1482
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 10723..20235

OTHER INFORMATION: /codon_start= 10723

OTHER INFORMATION: /function= "gene =erya"

OTHER INFORMATION: /product= "orf3 encoding modules 5 & 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1693..2670
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 10225..10483
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OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                                                                                                                                                                                        LOCATION: 19.4470
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 4471..10722
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /function= "approximate span OTHER INFORMATION: beta-ketoreductase of module 4"
ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 3406..3921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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OTHER INFORMATION: 6-deoxyerythronolide B formatio

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LOCATION:
RESULT 15
US-08-439-009A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 CTCTCCCTGCACACCGCCTGCGCAGCTCCAGCCCCTGCGGCTGACATGCGGAGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 CIGGACIGGAGIGACAGCCIGGCCCAACIGGCICAAGCCAGGGCAGCCCICIGIGGAAIC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 15172..16569
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 20235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Indels
                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 12379..1350
OTHER INFORMATION: Afunction= "approximatr span of
OTHER INFORMATION: acyltransferase domain of module 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 19149..19398
CHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 19492..20335
OTHER INFORMATION: /function= "approximate span of
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LOCATION: 14857..15114
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 15166.20235
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OTHER INFORMATION: module 6"
            NAME/KEY: misc_feature
LOCATION: 10723..13165
COCATION: //function= "approximate span of
OTHER INFORMATION: module 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LGCATION: 14062..14610
OTHER INFORMATION: Cfunction= "approximate span
OTHER INFORMATION: beta-ketoreductase of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.0%; Score 32.2; Dilarity 52.6%; Pred. No. 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 18379.18921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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Matches 70; Conserve
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/codon_start= 19
/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for
6-deoxyerythronolide B"
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LOCATION: 97..1482
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
                                                                            APPLICANT: Donadio, S
APPLICANT: Katz, L
APPLICANT: Mcalpine, J
APPLICANT: Mcalpine, J
APPLICANT: Mcalpine, Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1937..2670
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 19.4470
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 3"
                                                                                                                                                                                                                                     ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTE: 0.05

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439,009A

FILING DATE: 11-MAY-1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharopolyspora erythraea
Sequence 3, Application US/08439009A Patent No. 6004787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
LENGTH: 20235 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 19..10722
OTHER INFORMATION: /c
OTHER INFORMATION: /f
OTHER INFORMATION: /F
OTHER INFORMATION: 6-
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                   STATE:
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LOCATION: 4471...5847

OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacylACFsynhase domain of module"
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LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and enoylreductase domains m"
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LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoreductase domain of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /codon_start= 10723
OTHER INFORMATION: /function= "gene =eryA"
OTHER INFORMATION: /product= "orf3 encoding modules 5 & OTHER INFORMATION: 6-deoxyerythronolide B formatio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
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LOCATION: 12379..13350
OTHER INFORMATION: /function= "approximatr span of
OTHER INFORMATION: acyltransferase domain of module 5"
                                                                                                            LOCATION: 4171..4428
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 4"
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LOCATION: 9433..9984
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: beta-ketoreductase of module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 10723.15165
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 5"
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LOCATION: 14062..14610
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
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LOCATION: 15166..20235
OTHER INFORMATION: /function= "approximate span of
                                                                                      NAME/KEY: misc_feature LOCATION: 4171..4428
                                                                                                                                                                                                                                        misc_feature
4471..10722
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
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LOCATION:
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PERATURE:

NAME/KEY: misc_feature

LOCATION: 15172.156

OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"

NAME/KEY: misc_feature

COTHER INFORMATION: /function= "approximate span of other information: /function="approximate span of other information: /function="approximate span of other information: 1572.1521

OTHER INFORMATION: acyltransferase domain of module 6"

NAME/KEY: misc_feature

COCATION: 1879-1831

OTHER INFORMATION: /function= "approximate span of other information: /function="approximate span of other information: /
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(without alignments)
7656.298 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363474 seqs, 203117208 residues
                                                                                                                                                                                                                                                                                             US-09-944-896-49_COPY_201_447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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	c	19,	,61	16	,61	49,	49,	49,	49,	49,	49,	49,	49,	49,		49,		ì	12,	12,
	Description	Sequence 49	Sequence 4	Sequence 49	Sequence 49	Seguence	Sequence	Sequence 4	Seguence	Sequence	Sequence 3	Sequence	Sequence 12,	Sequence 12, Appl						
	ID	US-09-944-413-49	US-09-944-403-49	US-09-944-896-49	US-09-944-944-49	US-09-866-028-49	US-09-944-449-49	US-09-944-457-49	US-09-945-587-49	US-09-945-015-49	US-09-944-396-49	US-09-944-097-49	US-09-944-432-49	US-09-943-762-49	US-09-944-654-49	US-09-943-851A-49	US-09-790-264-3	US-09-790-264-1	US-10-042-141-12	US-09-726-643-12
		- 6	6	6	6	10	10	10	10	10	10	10	10	10	10	10	10	10	0	10
	Query Match Length DB	1876	1876	1876	1876	1876	1876	1876	1876	1876	1876	1876	1876	1876	1876	1876	1338	1856	1923	1923
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US-09-834-975-872 US-09-814-975-873 US-09-905-291A-284 US-09-909-320-284 US-09-909-320-284 US-09-909-320-284 US-09-999-735-360 US-09-989-735-360 US-09-989-725-360 US-09-989-725-360 US-09-989-725-360 US-09-989-723-360 US-09-989-727-360 US-09-989-727-360 US-09-989-727-360 US-09-989-727-360 US-09-989-727-360 US-09-991-163-360 US-09-991-173-360 US-09-991-173-360 US-09-991-173-360 US-09-991-173-360 US-09-991-173-360 US-09-991-173-360	
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ALIGNMENTS

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APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Hilan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE REFERENCE: P2544PICI
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
                            Sequence 49, Application US/09944113 Patent No. US20020156004A1
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Grimaldi, Christopher
Gurney, Austin
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Filvaroff, Ellen
                                                                           GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Goddard, Audrey
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US-09-944-413-49
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APPLICATION NUMBER: PCT/USS9/28409
FILING DATE: No. US20020156004Alember 30, 1999
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FILING DATE: No. US20020156004Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: POT/USOO/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: POT/USOO/08439
PRIOR FILING DATE: March 30, 2000
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PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/USOO/20710
PRIOR FILING DATE: July 28, 2000
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FILING DATE: December 16, 1999
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PRIOR APPLICATION NUMBER: PCT/0S00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
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                                                                                               PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR PILING DATE: December 18, 1998
PRIOR PILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR PILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: Pebruary 25, 1998
PRIOR FILING DATE: December 16, 1998
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PRIOR PILING DATE: Jecember 15, 1999
PRIOR PILING DATE: Jecember 16, 1999
PRIOR PILING DATE: Jecember 16, 1999
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PRIOR PILING DATE: Jecember 16, 1999
                                      FILLING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
APPLICATION NUMBER: 60/069,702
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NUMBER OF SEQ ID NOS: 120
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Matches 247; Conservative
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ORGANISM: Homo Sapien
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LENGTH: 1876
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201 GAGGIGIGCCCACCCCAGCIGCAGGAGCAGGCICCGAIGGCCGGAGCCCIGAACAGGAAG 260
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                                                                                                                                                                                                                                                                                                  181 GCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG
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FILE REFERENCE: P2548PIC1
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CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR PELING DATE: DECEMBER: 0/06/334
PRIOR FILING DATE: DECEMBER: 1, 1997
PRIOR APPLICATION NUMBER: 60/06/335
PRIOR APPLICATION NUMBER: 60/06/36/35
PRIOR APPLICATION NUMBER: 60/06/376
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR APPLICATION NUMBER: 60/06/9/425
PRIOR APPLICATION NUMBER: 60/06/9/425
PRIOR APPLICATION NUMBER: 60/06/9/425
PRIOR APPLICATION NUMBER: 60/06/9/702
PRIOR APPLICATION NUMBER: 60/06/9/702
PRIOR PELING DATE: DECEMBER 16, 1997
PRIOR PELING DATE: DECEMBER 16, 1997
PRIOR PELING DATE: DECEMBER 17, 1997
PRIOR APPLICATION NUMBER: 60/06/9/873
PRIOR PELING DATE: DECEMBER 17, 1997
PRIOR APPLICATION NUMBER: 60/06/9/873
PRIOR PELING DATE: DECEMBER 17, 1997
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
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Patent No. US20020165143A1
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Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Napier,Mary
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Godowski, Paul
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Tumas, Daniel
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                                                         241 GGCTGGA 247
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US-09-944-896-49
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020165143Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020165143Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
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                    DR FILING DATE: February 9, 1998

DR APPLICATION NUMBER: 60/075,945

DR APPLICATION NUMBER: 60/112,850

DR FILING DATE: December 16, 1998

PRELING DATE: December 22, 1998

PRELING DATE: December 22, 1998

DR APPLICATION NUMBER: 60/113,296

DR FILING DATE: December 22, 1998

RAPLICATION NUMBER: 60/146,222

DR FILING DATE: September 16, 1998

RELING DATE: September 16, 1998
                                                                                PRIOR FILING DATE: FEBICARY 25, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR PELIORATION NUMBER: PCT/US98/1930
PRIOR PELIORATION NUMBER: PCT/US98/1930
PRIOR PELIORATION NUMBER: O9/216,021
PRIOR PELIOR DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 12, 1998
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PRIOR PELING DATE: December 16, 1999
PRIOR PELING DATE: PERIOR 30/254,311
PRIOR PELING DATE: September 15, 1999
PRIOR PELING DATE: September 16, 1999
PRIOR PELING DATE: December 11, 2000
PRIOR PELING DATE: PEDICATION NUMBER: PCT/US09/280/0414
PRIOR PELING DATE: PEDICATION NUMBER: PCT/US00/0414
PRIOR PELING DATE: FEBICARY 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0419
PRIOR PELING DATE: PEDICARY 11, 2000
PRIOR PELING DATE: PEDICARY 11, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR PELING DATE: POWENTER PCT/US00/20710
PRIOR PELING DATE: POWENTER PCT/US00/32678
PRIOR PELING DATE: POWENTER PCT/US00/32678
PRIOR PELING DATE: PEDICATION NUMBER: PCT/US00/32678
PRIOR PELING DATE: PEDICATION NUMBER: PCT/US00/32678
PRIOR PELING DATE: PEDICATION NUMBER: PCT/US00/32678
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Best Local Similarity 100.0
Matches 247; Conservative
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LENGTH: 1876
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APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                              ACIDS ENCODING THE SAME
                                                                                                                               FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
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APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
                                                                                                                                                                                                           CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: EEDTUARY 9, 1998
PRIOR FILING DATE: FEBTUARY 9, 1998
PRIOR FILING DATE: FEBTUARY 25, 1998
PRIOR FILING DATE: PEDTUARY 25, 1998
PRIOR FILING DATE: PEDTUARY 26, 1999
PRIOR FILING DATE: PEDTUARY 25, 1998
PRIOR FILING DATE: PEDTUARY 26, 1999
PRIOR PELICATION NUMBER: 60/116, 298
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020173463Alember 30, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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APPLICATION NUMBER: PCT/US98/19330
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PRIOR PELING DATE: December 3, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR PRILING DATE: December 17, 1998
PRIOR FILING DATE: PEDRUARY 9, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 17, 1999
PRIOR FILING DATE: PROPERMER: 09/216,021
PRIOR APPLICATION NUMBER: 07/US98/2109
PRIOR FILING DATE: PROPERMER: 09/216,021
PRIOR APPLICATION NUMBER: PCT/US98/2109
PRIOR FILING DATE: MATER 3019
PRIOR FILING DATE: PROPERMER: PCT/US98/2109
PRIOR FILING DATE: PORTIOR DATE: PORTIOR DATE: PROPERMER 16,1999
PRIOR FILING DATE: PORTIOR DATE: PORTIOR DATE: PORTIOR DATE: PROPERMER 16,1999
PRIOR FILI
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Grimaldi, Christopher
                        Ferrara, Napoleone
Filvaroff, Ellen
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                                                                                         Gerritsen, Mary
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Napier,Mary
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Eaton, Dan
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                 PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999
PRIOR PELING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020168715Alember 30, 1999
PRIOR FILING DATE: No. US20020168715Alember 30, 1999
PRIOR FILING DATE: No. US20020168715Alember 30, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR PRILING DATE: December 1, 2000
PRIOR PRILING DATE: PECT/US99/28301
PRIOR PRILING DATE: PECT/US99/28409
PRIOR PRILING DATE: PECHUARY 11, 2000
PRIOR FILING DATE: PECPLUARY 11, 2000
PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: PEPURARY 22, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 28, 2000
PRIOR FILING DATE: MAY 28, 2000
PRIOR FILING DATE: JULY 28, 2000
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100.0%; Pred. No. 1.2e-54;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/US00/332678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
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Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: BAKET, KEVIN
APPLICANT: BOLSTEIN, David
PRIOR APPLICATION NUMBER: 09/216,021
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Matches 247; Conservative
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US-09-944-896-49
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LENGTH: 1876
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US-09-944-944-49
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT APPLICATION NUMBER: US/09/866,028
FILE REFERENCE: 2001-05-25
PILOT APPLICATION OF SEQ ID NOS: 120
SEQ ID NO 49
ILOTH: 1876
TYPE: DNA
CORGANISM: HOMO Sapien
US-09-866-028-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 GAGAGTTCTTGTTGTTCTCCTCCTGCACAACCGCCTGCGCAGGTGGGTCCAGCCCCTGCG 320
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CURRENT APPLICATION NUMBER: US/09/944,449
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 60/667,411
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PRIOR APPLICATION WNBRER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/06935
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Patent No. US20020102647A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grimaldi, Christopher
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APPLICANT: Botstein, David
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Goddard, Audrey
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                                             Wood, William
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                            Tumas,Daniel
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Napier, Mary
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Wood, William
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Best Local Similarity
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020173463Alember 30, 1999
PRIOR PILING DATE: No. US20020173463Alember 30, 1999
PRIOR PLING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 11, 2000
PRIOR PILING DATE: February 11, 2000
PRIOR PILING DATE: February 22, 2000
PRIOR PILING DATE: February 22, 2000
PRIOR PLING DATE: PCT/US00/06841
PRIOR PLING DATE: MATCH 2, 200
PRIOR PAPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/2678
PRIOR PILING DATE: MATCH 30, 2000
PRIOR PILING DATE: MATCH 30, 2000
PRIOR PILING DATE: MATCH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR PILING DATE: FEBTUARY 28, 2001
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Patent No. US20020058309A1
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Filvaroff, Ellen
Gerritsen, Mary
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DARIE: February 9, 1998
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PRIOR PLING DARE: February 25, 1998
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PRIOR FILING DARE: September 22, 1998
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PRIOR PRILING DARE: No. US20020102647Alember 30, 1999
PRIOR PRILING DARE: No. US20020102647Alember 30, 1999
PRIOR PAPLICATION NUMBER: PCT/US99/2009
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PRIOR PLING DARE: No. US20020102647Alember 30, 1999
PRIOR PRILING DARE: PEDENDARY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: PCT/US00/0416
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APPLICATION NUMBER: 60/070,440
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                                                                                                                FILING DATE: December 12, 1997 APPLICATION NUMBER: 60/069,696
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                                                        FILING DATE: December 11, 1997 APPLICATION NUMBER: 60/069,425
FILING DATE: December 11, 1997
                         APPLICATION NUMBER: 60/069,278
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                                                  Length 1876;
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                                                  100.0%; Score 247; DB 10;
100.0%; Pred. No. 1.2e-54;
iive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/66,411
PRIOR APPLICATION NUMBER: 60/66,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PLING DATE: December 11, 1997
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APPLICATION NUMBER: 60/069,702
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Goddard, Audrey
Godowski, Paul
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Hillan, Kenneth
                                                                                             Conservative
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APPLICANT: Botstein, David
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Wood, William
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; ORGANISM: Homo Sapien
US-09-944-449-49
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Best Local Similarity
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441 GGCTGGA 447
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/945,587

CURRENT APPLICATION NUMBER: 09/866,028

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-26

PRIOR FILING DATE: 2001-05-26
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PRIOR APPLICATION NUBBER: 60/067 411
PRIOR PILING DATE: December 3, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUBBER: 60/069335
PRIOR FILING DATE: December 11, 1997
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Patent No. US20020127643A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/069,596
APPLICATION NUMBER: 60/069,694
APPLICATION NUMBER: 60/069,694
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FILING DATE: December 17, 1997
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APPLICATION NUMBER: 60/068,017
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Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Hillan, Kenneth
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FILING DATE: NO. US20002110859Alember 30, 1999
FILING DATE: NO. US20020110859Alember 30, 1999
FILING DATE: NO. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
APPLICATION NUMBER: PCT/US99/28301
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/USO/20710
APPLICATION NUMBER: PCT/USO/32678
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
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DR APPLICATION NUMBER: 60/074,092
DR FILING DATE: February 9, 1998
DR APPLICATION NUMBER: 60/075,945
DR FILING DATE: February 25, 1998
DR PAPLICATION NUMBER: 60/112,850
DR FILING DATE: December 16, 1998
DR APPLICATION NUMBER: 60/112,296
DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 60/145,222
DR FILING DATE: December 22, 1998
                                                                                                     FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
                                                                                                                                                       FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
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FILING DATE: December 16, 1998
                                                                   APPLICATION NUMBER: 60/068,017
                         APPLICATION NUMBER: 60/069,87;
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  December 17,
                                               FILING DATE: December 17
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NUMBER OF SEQ ID NOS: 120
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ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: 60/074,092 PRIOR FILING DATE: February 9, 1998 PRIOR APPLICATION NUMBER: 60/075,945

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FILLING DATE: February 25, 1998 APPLICATION NUMBER: 60/112,850

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APPLICATION NUMBER: 09/216,021
                                                                                                                           Sequence 49, Application US/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                       Grimaldi,Christopher
                                                                                                                                                                                                                                                                                              Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Hillan, Kenneth
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                                                                                                       US-09-945-015-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020127643Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020127643Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 13, 1999
PRIOR FILING DATE: December 13, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. US20020127643Alember PRIOR FILING DATE: No. US20020127643Alember PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 16, 1999
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PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PROTUNS99/28301
PRIOR FILING DATE: PEDRUARY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: PEDRUARY 22, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDRUARY 22, 2001
                                                                                                                                   FILING DATE: JULY 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PILING DATE: December 22, 1998
PRIOR FILING DATE: JOHN 28, 1999
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: JOHN 28, 1999
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 16, 1998
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Best Local Similarity 100.(
Matches 247; Conservative
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; ORGANISM: Homo Sapien
US-09-945-587-49
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LENGTH: 1876
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                              THILE OF INVENTION: ACLIDS ENCOLING THE SAME
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT APPLICATION NUMBER: US/08/028
PRIOR APPLICATION NUMBER: US/06/028
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR PILING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 16, 1997
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PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 17, 1997
PRIOR FILING DATE: DECEMBER 18, 1997
PRIOR FILING DATE: FEBRUARY 5, 1998
PRIOR FILING DATE: FEBRUARY 25, 1998
PRIOR FILING DATE: PEBRUARY 25, 1998
PRIOR FILING DATE: PECCEMBER 16, 1999
PRIOR FILING DATE: DECEMBER 20,113, 296
PRIOR FILING DATE: DEC
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APPLICATION NUMBER: PCT/US08/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PELICATION NUMBER: 60/069,334
PRIOR PELICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PLILNG DATE: December 11, 1997
PRIOR PLILNG DATE: December 12, 1997
PRIOR PLILNG DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR PELING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,870
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PRIOR APPLICATION NUMBER: 60/069,870
PRIOR PELING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR APPLICATION NUMBER: 60/070,40
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: DECEMBER 16/10599/12352
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CURRENT FILING DATE: 2001-09-26
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APPLICATION NUMBER: PCT/US99/28409
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Grimaldi, Christopher
                                          Filvaroff, Ellen
Gerritsen, Mary
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Napier, Mary
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Wood, William
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                                                                                                                OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/1252
OR APPLICATION NUMBER: PCT/US99/1209
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR FILING DATE: No. US20020132768Alember 30, 1999
                                       PRIOR APPLICATION NUMBER: 09/218,517
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR PLILNG DATE: March 3, 1999
PRIOR PLILNG DATE: JUBBER: PCT/US99/1252
PRIOR PELICATION NUMBER: PCT/US99/28409
PRIOR PLILNG DATE: PCCCOS99/28409
PRIOR PELING DATE: NO. US20020132768Alember
PRIOR PLILNG DATE: DECEMBER: PCT/US99/28301
PRIOR PLILNG DATE: DECEMBER: PCT/US99/28301
PRIOR PLILNG DATE: DECEMBER: PCT/US99/3005
PRIOR PLILNG DATE: PEDLUATY 11, 2000
PRIOR PLILNG DATE: FEDLUATY 22, 2000
PRIOR PELICATION NUMBER: PCT/US00/0841
PRIOR PLILNG DATE: FEDLUATY 22, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR PELING DATE: MAY 22, 2000
FILING DATE: December 16, 1998
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NUMBER OF SEQ ID NOS: 120
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Patent No. US20020132981A1
GENERAL INFORMATION:
                                APPLICATION NUMBER: 09/218,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 247; Conservative
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-945-015-49
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Best Local Similarity
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LENGTH: 1876
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g δλ q Qγ g òγ q δ qq

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CURRENT APPLICATION NUMBER: US/09/944,097
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/86,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
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FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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FILING DATE: June 22, 1999
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PLILONION NUMBER: 60/069,278
PRIOR PLILON DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PRIOR DATE: December 17, 1997
PRIOR PRIOR DATE: December 17, 1997
PRIOR PLING DATE: December 17, 1997
PRIOR PLING DATE: December 17, 1997
PRIOR PLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR PLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,017
PRIOR APPLICATION NUMBER: 60/069,017
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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Wood, William
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   No. US20020132981Alember 30, 1999
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                     PRIOR APPLICATION NUMBER: PCT/US99231ALTENDEL PRIOR FILING DATE: December1, 1999
PRIOR FILING DATE: December1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: Pebruary 22, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: JUJY 28, 2000
PRIOR FILING DATE: JUJY 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEBROR PCT/US00/32678
PRIOR FILING DATE: PEBROR PCT/US00/32678
PRIOR FILING DATE: PECEMBER 1, 2000
PRIOR FILING DATE: PEBROR 1, 2001
PRIOR FILING DATE: PEBROR PCT/US01/06520
PRIOR FILING DATE: PEBROR PCT/US01/06520
PRIOR FILING DATE: PEBROR PCT/US01/06520
PRIOR PRIOR FILING DATE: PEBROR PCT/US01/06520
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Grimaldi, Christopher
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Best Local Similarity 100.0
Matches 247; Conservative
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APPLICANT: Botstein, David
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Roy, Margaret
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ORGANISM: Homo Sapien
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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APPLICATION NUMBER: PCT/VS99/228409
FILING DATE: NO. US20020134675Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/USO0/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/USO0/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/USO0/14042
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APPLICATION NUMBER:
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ORGANISM: Homo Sapien
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APPLICANT: GOGOWSKI, Paul
APPLICANT: GUTMEY, Austin
APPLICANT: GUTMEY, Austin
APPLICANT: GUTMEY, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Nijavin, Ivar
APPLICANT: Noy, Margaret
APPLICANT: Noy, Margaret
APPLICANT: FOY, Margaret
APPLICANT: FOY, Margaret
APPLICANT: Wood, William EN
APPLICANT: Wood, William EN
APPLICANT: Wood, William EN
APPLICANT: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P2248PICI
GURRENT APPLICATION NUMBER: US/09/944,432
                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Score 247; DB 10; Length 1876;
Best Local Similarity 100.0%; Pred. No. 1.2e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0;
PRIOR FILING DATE: MAY 22, 2000
PRIOR APPLICATION UNBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
LENGTH: 1876
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PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR PRICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
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Patent No. US20020142419A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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APPLICANT: Botstein, David
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US-09-944-097-49
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Best Local Similarity
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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020142419Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020142419Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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PRIOR PILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
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PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: DECEMBER: PCT/US99/28409
PRIOR PILING DATE: DECEMBER 17, 1999
PRIOR PILING DATE: DECEMBER 1, 1999
PRIOR PILING DATE: DECEMBER 1, 1999
PRIOR PILING DATE: DECEMBER 1, 1999
PRIOR PILING DATE: PEDIUARY 11, 2000
PRIOR PILING DATE: PEDIUARY 22, 2000
PRIOR PAPLICATION NUMBER: PCT/US00/O8419
PRIOR PILING DATE: MATCH 3, 2000
PRIOR PAPLICATION NUMBER: PCT/US00/O8419
PRIOR PILING DATE: MATCH 3, 2000
PRIOR PAPLICATION NUMBER: PCT/US00/20710
PRIOR PAPLICATION NUMBER: PCT/US00/20710
PRIOR PILING DATE: MATCH 30, 2000
PRIOR PAPLICATION NUMBER: PCT/US00/20710
PRIOR PILING DATE: MATCH 30, 2000
PRIOR PAPLICATION NUMBER: PCT/US00/20710
PRIOR PILING DATE: DECEMBER 1, 2000
PRIOR PAPLICATION NUMBER: PCT/US00/20710
PRIOR PILING DATE: DECEMBER 1, 2000
PRIOR PILING DATE: PEDIUARY 28, 2001
NUMBER OF SEQ ID NOS: 120

SEQ ID NO 49

LENGTH: 1876
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APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
                                                              PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR FILING DATE: December 19, 1997
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APPLICATION NUMBER: 60/074,092
FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,425
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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                                                                                      Gaps
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                                  Length 1876;
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                                     100.0%; Score 247; DB 10;
100.0%; Pred. No. 1.2e-54;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-09-26
PRIOR PPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: December 3, 1997

PRIOR PELING DATE: December 3, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

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PRIOR PILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069, 702

PRIOR PILING DATE: December 16, 1997

PRIOR PILING DATE: December 17, 1997
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Patent No. US20020142958A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
                                            Query Match 100.0
Best Local Similarity 100.0
Matches 247; Conservative
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Hillan, Kenneth
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APPLICANT: Botstein, David
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Tumas, Daniel
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US-09-944-432-49
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61 GAGAGTTTCTTGCTCCTCTCCTGCACACCGCCTGCGCAGCTGGGTCCAGCCCCTGCG 120
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                                                                                       PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: JANUARY 5, 1998
PRIOR FILING DATE: JANUARY 5, 1998
PRIOR FILING DATE: JANUARY 5, 1998
PRIOR PELICATION NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR PELICATION NUMBER: 60/112,850
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PELICATION NUMBER: 60/113,296
PRIOR PELICATION NUMBER: 60/113,296
PRIOR PELICATION NUMBER: 60/113,296
PRIOR PELICATION NUMBER: 60/116,296
PRIOR PELICATION NUMBER: 60/146,222
PRIOR PELICATION NUMBER: 60/216,021
PRIOR PELICATION NUMBER: 60/216,021
PRIOR PELICATION NUMBER: 60/216,311
PRIOR PELICATION NUMBER: 60/2099/28313
PRIOR PELICATION NUMBER: 60/2099/28313
PRIOR PELICATION NUMBER: 60/200142958Alember 30, 1999
PRIOR PELICATION NUMBER: 60/200142958Alember 30, 1999
PRIOR PELICATION NUMBER: 60/2009/2858
PRIOR PELICATION NUMBER: 60/2009/2858
PRIOR PELICATION NUMBER: 60/2009/2858
PRIOR PELICATION NUMBER: 60/2009/2858
PRIOR PELICATION NUMBER: PCT/US99/2809
PRIOR PELING DATE: DECEMBER! 1, 2000
PRIOR PELING DATE: PEDLICATION NUMBER: PCT/US99/2809
PRIOR PELING DATE: PEDLICATION NUMBER: PCT/US99/2809
PRIOR PELING DATE: PEDLICATION NUMBER: PCT/US99/2809
PRIOR PELING DATE: PEDLICATION NUMBER: PCT/US90/0414
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100.0%; Pred. No. 1.2e-54;
tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
LENGTH: 1876
FILING DATE: December 17, 1997
APPLICATION UNDBER: 60/068, 017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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Best Local Similarity
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                                                                         181 GCCCTCTGTGGAATCCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTG 240
261 GAGAGITICTIGCTCCTCTCCTGCACAACGCCTGCGAGCTGGGTCCAGCCCCCTGCG 320
                                                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/944,654
CURRENT FILING DATE: 2001-09-26
REIGN FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 1, 1997
PRIOR FILING DATE: December 1, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 973
PRIOR APPLICATION NUMBER: 60/069, 973
PRIOR APPLICATION NUMBER: 60/0704, 440
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/0704, 409
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/0704, 092
PRIOR APPLICATION NUMBER: 60/0704, 092
PRIOR APPLICATION NUMBER: 60/0704, 092
PRIOR FILING DATE: PEDLUARY 5, 1998
PRIOR APPLICATION NUMBER: 60/0704, 092
PRIOR APPLICATION NUMBER: 60/0704, 092
PRIOR FILING DATE: FEDLUARY 9, 1998
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APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
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Patent No. US20020142959A1
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Grimaldi, Christopher
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Hillan, Kenneth
Kljavin, Ivar
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GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Wood, William
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Roy, Margaret
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FRIOR FILING DATE: December 1, 1998
FRIOR APPLICATION NUMBER: 09/216,021
FRIOR APPLICATION NUMBER: 09/216,021
FRIOR APPLICATION NUMBER: 09/218,517
FRIOR APPLICATION NUMBER: 09/218,517
FRIOR FILING DATE: December 22, 1998
FRIOR FILING DATE: March 3, 1999
FRIOR FILING DATE: March 3, 1999
FRIOR FILING DATE: June 22, 1999
FRIOR FILING DATE: June 22, 1999
FRIOR APPLICATION NUMBER: PCT/US99/2813
FRIOR APPLICATION NUMBER: PCT/US99/28313
FRIOR APPLICATION NUMBER: PCT/US99/28301
FRIOR APPLICATION NUMBER: PCT/US09/4014
FRIOR APPLICATION NUMBER: PCT/US09/4014
FRIOR FILING DATE: December 1, 1999
FRIOR FILING DATE: February 11, 2000
FRIOR FILING DATE: February 22, 2000
FRIOR FILING DATE: February 22, 2000
FRIOR FILING DATE: MATCh 30, 2000
FRIOR FILING DATE: FEBRUARY 22, 2000
FRIOR FILING DATE: FEBRU
                                                                  PRIOR APPLICATION NUMBER: 60/113.296
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 1, 1998
APPLICATION NUMBER: 60/112,850
                                              December 16, 1998
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441 GGCTGGA 447

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APPLICANT: Wood, William TTTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED ENCODING THE SAME FILE REPERENCE: P2548P1C1 CURRENT APPLICATION NUMBER: US/09/943,851A
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FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR PILING DATE: December 17, 1998
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PRIOR PILING DATE: December 17, 1998
PRIOR PILING DATE: PEDRUATY 9, 1998
PRIOR PILING DATE: PEDRUATY 9, 1998
PRIOR PILING DATE: PEDRUATY 9, 1998
PRIOR PILING DATE: PEDRUATY 25, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PILING DATE: DECEMBER 16, 113, 296
PRIOR PILING DATE: SEPTUATY 9, 1998
PRIOR PILING DATE: DECEMBER 16, 113, 296
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PRIOR APPLICATION NUMBER: US/09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PLICATION NUMBER: 60/067,411
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
                                                         Sequence 49, Application US/09943851A Patent No. US20020150976A1 GENERAL INFORMATION:
APPLICANT: Baker, Kevin APPLICANT: Botstein, David
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PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
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PRIOR FILING DATE: No. US20020150976Alember 30, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: February 11, 2000
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PRIOR FILING DATE: February 22, 2000
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PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: JULY 28, 2000
PRIOR PILING DATE: December 1, 2000
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CRGANISM: Homo Sapien
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                 - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                 coding for human PRO347 (UN0306) (see AAY06482). The clone was isolated from a foetal kidney library. Amplification of DNA44176 occurs in various tumours, suggesting an association with tumour formation or growth. Antagonists (e.g. antibodies) directed against PRO347 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may be useful targets for the diagnosis and/or treatment (including prevention)
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                                                                                                                                                                                                                                    Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment
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                                                                                                                                                   Gurney AL, Hillan KJ, Lawrence DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;
                                                                                                                                                                                                                                                                               Example 1; Fig 13; 162pp; English:
                                    980S-070440.
980S-0083500.
980S-0086414.
980S-0088742.
                           98US-0109304
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Best Local Similarity 100.
Matches 1876; Conservative
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05-JAN-1999;
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10-JUN-1998;
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                                                                                                                                                                                                                                                                                    Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder; ss.
          Nucleic acids encoding PRO secreted and transmembrane proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney AL,
                                                                                                                                                                                                                                                                    Human PRO347 nucleotide sequence.
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       The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a novel human polypeptide. The Specification describes novel polypeptides designated PRO201, PRO292, PRO347, PRO157, PRO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-polypeptide antibody useful in the treatment and diagnosis of plastic cell growth and proliferation .
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described. The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                          New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCC
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                                                                                                                                                                                Eaton DL, Ferrara N, Filvaroff E;
,, Godowski PJ, Grimaldi CJ, Gurney AL,
Napier MA, Roy MA, Tumas D, Wood WI;
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                            Napier MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 19; 187pp; English.
                                          98WO-US25108.
98US-0112850.
98US-0113296.
99WO-US28301
                                                                                                                                                                                                         Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 1876; Conservative
                                                                                                                                                                                                                     Kljavin IJ,
                                                                                                                                                                                  Botstein D,
                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                       and diagnostic agents
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us-09-944-896-49.olil0.rng

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cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopolesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; contraceptic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/product= "Mature human protein with hydrophobic domain"
                                                                                                                                       Human proteins with hydrophobic domains and the nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
62..142
                                                                                                                                                                                                                                                                                                                                        Human protein having hydrophobic domain encoding cDNA clone HP10760
AATGCCAGAAGTTGGGCAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGATT
                                             AGAAGAAGCTGGGGCCCTTCGCCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGC
                                                                                          GAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCC
                                                                                                                                                                                                                                                                                                                                                              hydrophobic domain; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
62..1402
/*tag= a
/product= "Human prot
                                                                                                                                                                                                                                                                    AAD12570 standard; cDNA; 1775 BP.
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(SAGA ) SAGAMI CHEM RES CENT.
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2000JP-0002299.
2000JP-0026862.
2000JP-0058367.
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                                                                                                                                                                                                  CTGAAAAAAAAAAA 1876
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143..1399
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11-JAN-2000; 2
03-FEB-2000; 2
03-MAR-2000; 2
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1621
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The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10760. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The colypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and in assays to identify modulaters of polypeptide expression and call proliferation activity, to modulate cytokine and cell proliferation activity, to modulate tissue growth activity (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, theumatodia arthritis and insulin-dependent diabetes), to modulate tissue growth activity (e.g. for the chaematopoiesis, to modulate tissue growth activity (e.g. for controlling fartility), to modulate activity and inhibin activity (e.g. for controlling fartility), to modulate chemotactic and chemokinetic activity, to modulate receptor controlling activity, to modulate receptor controlling activity, to modulate thrombolytic activity, to modulate receptor controlling activity, to modulate inflammation and to inhibit tumour growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGACGGGCCCAACAGACCCATGCTGCATCCAGAGCTCCCCTGGCCGGGGGGCATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 CTGGCTGTGCTCCTGGCCCTCCTTGGCACCTGGGCAGAGGTGTGGCCACCCCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACAGCCACGCGGCAGGAGTGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTC
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them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
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99.7%; Pred. No. 0;
11ve 0; Mismatches
                                                                                      Claim 4; Page 271-275; 563pp; English.
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Best Local Similarity 99.7
Matches 1229; Conservative
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g ò В ò g Ω Dp ò αq δ g ò g ò qq Qγ g

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Human; T139 polypeptide; immune system disorder; spermatogenesis; ss; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1242 ACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACC 1301
             941
                                               821
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                                                                                                           TCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTG
                                                                                                                                                                                                                                                                                                                                      CTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCCTTCTATCTGGGCCGCCTG
702 ACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGC
                                                            GGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTC
                                                                                                                                                                                                                881 CGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACC
                                                                                                                                                                                                                                        AAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTG
                                               TGCTTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGC
                                                                                             822 ATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1241 AGTTTTGCCTTTGGCAGCCTGACAACCACGGG 1273
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/product= "T139 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human T139 protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ23299 standard; cDNA; 1856
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GTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACA

461

582

521

642 581

GTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCACCTGTGCTGCTGCAGGCCAGGCA GCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAG

520 641

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Holtzman D;

WPI; 1999-633969/54

P-PSDB; AAY41266.

Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression or activity .

Claim 2; Fig 1; 115pp; English.

This cDNA encodes a human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 CDNA insert is deposited with ATCC under accession number 98694. The T139 polypeptides and polynucleotides can be administered therapeutically or activity, especially proliferative or differentiative cypression or activity, especially proliferative or differentiative disorders, e.g. of the immune system. They can be used to modulate spermatogenesis, e.g. as a contraceptive to decrease spermatogenesis or to treat disorders related to defects in sperme egg fusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively binding compounds which may be useful for detecting the polypeptides; and identifying compounds modulating polypeptide activity. The polynucleotides are useful for producing probes or primers that selectively hybridize to the polynucleotides which may be useful for detecting the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant T139 levels; determining if a gene has been mutated or deleted to may level; and for monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate /prevent T139 expression.

Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;

; 0 493 74 CCTGACGGGCCCAACAGACCCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGGATCTC 133 253 373 221 CTGCACACACCGCCTGCGCAGCTGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGAC 341 374 ccGAGCCTGGCGTCCGGCCTGTGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGCTG 433 CCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGCAGCGG 521 102 CCTGACGGGCCCAACAGACCCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGGCATCTC 161 134 CTGGCTGTGCTCCTGGCCCTCCTTGGCACCGCCTGGGCAGAGGTGTGGCCACCCCAGCTG 193 TGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACC 401 CCGAGCCTGGCATCCGGCCTGTGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTG 461 Gaps CTGGCTGTGCTCCTGGCCCTCCTTGGCACCACCTGGGCAGAGGTGTGCCCCACCCCAGCTG 434 CCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAGCCCTATGGTTTGCAGAGGGGCAGCGG Score 1029; DB 20; Length 1856; Pred. No. 0; Indels 4 0; Mismatches 54.98; 99.78; Matches 1229; Conservative Best Local Similarity 162 222 282 254 342 462 402 δý Op óγ qq òγ g ŏ g ò Q δ Q δ g

Db

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glomerular disease; glomerulonephritis, uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; haemostatic; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic; cytostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilliser; hypotensive; tumour; injury; trauma; antianginal; vasotropic; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; haematopoiesis; clotting; kidney failure; wound healing; cancer; neoplasis; panoreatic disorder; panoreatitis; cerebrovascular disease; heart disorder; ischemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive;
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                  GCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAG
                                                                                      ATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCT
                                                                                                                                                                                                                                                                                                                794 ATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCT
582 GTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACA
                                                                                                                                         ACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGC
                                                                                                                                                                        674 ACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGC
                                                                                                                                                                                                           TGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGC
                                                                                                                                                                                                                                            734 TGCTTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGC
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The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 crumurine WDNM-2, having diagnostic, preventive, (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability to modulate cell-cell interactions, haematopoiesis and the ability to modulate clotting. Polypeptide and polymucleotide of the invention are useful for diagnosing and treating disorder characterised by their aberrant expression or activity. The antibodies are useful as modulating agents in regulating a variety of cellular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful for treating defects such as kidney failure, TANGO-125 is useful in wound healing and for treating cancer, TANGO-110 creating cancer, are useful to treat pancreatic disorders, such as content disease, cardiovascular disease, and tumnours, and injury or traumance heart disease. cardiovascular disease, and tumnours, and injury or treating chomeroulonephritis), TANGO-139, 125, 110, 175 molecules are useful to treat crone chomic pheart disease, cardiovascular disease (e.g., acute and choner disease. TANGO-139, 125, 110 and 175 molecules are useful to treat crone choner disease. TANGO-139, 125, 110 and 175 molecules are useful to treat crone choner disease. TANGO-139, 125, 110 and 175 molecules are useful to treat crone choner disease. Cardiovascular associated diseases and disorder. TANGO-125 treats prostate disorders, such as inflammatory diseases, Crohn's.
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                              nepatotropic; antipsoriatic; antiallergic; dermatological; virucide;
cardiant; renal disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human mature T139 protein"
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95.1432
/*tag= d
/note= "This region designated as S
/...ffcally referred in claim 27"
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/product= "Human T139 protein"
95..172
apoptotic disorder; rheumatoid arthritis;
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                                                                                                                                                                                            Location/Qualifiers
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98US-0065661.
98US-0102705.
98US-0124538.
99US-0298531.
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(GOOD/) GOODEARL A D J.
(MCCA/) MCCARTHY S A.
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                                                             T139; gene; ss.
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22-JUN-1999;
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disease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for treating proliferative disorders, inflammatory disorders. TANGO-175, or WDNM-2 activity also include apoptotic disorders, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, immune-related disorders, e.g., immunodeficiency disorders, viral disorders, cell growth disorders, e.g., cancers and inflammatory disorders and apoptotic disorders. The nucleic acids of the invention are used in gene therapy. The present sequence is human T139 cDNA.
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                                                                                                                                                           Score 1029; DB 24; Length 1856;
Pred. No. 0;
0; Mismatches 4; Indels 0;
                                                                                                                                    Sequence 1856 BP; 402 A; 560 C; 564 G; 330 T; 0 other;
                                                                                                                                                               54.9%;
99.7%;
                                                                                                                                                                                           Matches 1229; Conservative
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                                                                                                                                                                             1094 CTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTG 1153
                              1002 AAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTG 1061
proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and anyolving abnormal anglogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful e.g.
promoting wo
                                           TCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTG
                                                                                                                                                 CTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to 26 secreted human proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 26 human secreted polypeptides, preventing, diagnosing and/or treating cancers and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF24152 standard; DNA; 1923
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                                                                                           102 CCTGACGGGCCCAACAGACCCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTC 161
                                                                      Gaps
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                                             DB 22; Length 1923;
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                      Sequence 1923 BP; 444 A; 568 C; 569 G; 342 T; 0 other;
                                                                    4;
                                                                   0; Mismatches
                                                         Pred. No. 0;
                                             Score 1029;
                                             54.98;
99.78;
                                                                      Matches 1229; Conservative
                                                         Local Similarity
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Tilly polypeptide can be expressed by standard recombinant methodology.

The Tilly polypeptide and be systemed accession number of the Tilly polypeptides and polynucleotides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant Tilly expression or activity, especially proliferative or disorders, e.g. of the immune system. They can be used to modulate spermatogenesis, e.g. of the immune system. They can be used to contact some to treat disorders related to defects in sperm-egg spermatogenesis or to treat disorders related to defects in sperm-egg tision. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively binding compounds which may be useful for detecting the polypeptides in selectively hybridize to the polynucleotides or primmers that selectively hybridize to the polynucleotides which may be useful for detecting the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant Tilly levels; determining if a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; T139 polypeptide; immune system disorder; spermatogenesis; ss; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping.
1079 TCTTCAGAGGCAGACACTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTG 1138
                                                          1181
                                                                        1182 GAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTC 1241
                                                                                                                                                  1259 ACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGGCCTTCACC 1318
                                                                                                                                                                                                      ACCIACAAGACCGCCAAGGACICCIIICCGCIGGGCCACAGGGGAGCACCAGGCCIICACC 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This represents the coding sequence of the human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology
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                                                      CTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCCTTCTATCTGGGCCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human T139 protein coding sequence.
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has been mutated or deleted to identify subjects at risk for or having disorder associated with T139 expression or activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate/prevent T139 expression.
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                                                                   Sequence 1338 BP; 259 A; 420 C; 413 G; 246 T; 0 other;
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0; Mismatches
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Sequence 1786 BP; 361 A; 548 C; 553 G; 324 T; 0 other;

SO

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The invention relates to primers for synthesising full length cDNA clones, 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human cDNA of the invention.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                               1083 TACAGAGCCAGGATGAAATGTCAGAGGAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1142
                                                                                                                1021 AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGATT 1080
                                                                                                                                                                                     1263 TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGCCT 1322
                                                           961 TACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAG 1020
                                                                                                AAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGACT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation \mbox{\, -}
901 ACCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTAT 960
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T, Koqa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 2850; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; full length cDNA; cDNA synthesis; oligo-capping;
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human full-length cDNA, SEQ ID NO: 2850
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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                                                                                                                                 342 TGGAGTGACAGCCTGGCCCAACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACC
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                       Indels
                      6
  22;
   DB
                      0; Mismatches
Score 774;
Pred. No. 0;
 41.3%;
illarity 99.3%;
Conservative
           Local Similarity
                      Matches 1224;
   Query Match
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO

diagnostic coding sequences of the invention.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as for foods supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. Che polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                  1241
 1181
               1191
                                                                                                                                                 ACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACC 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                   CTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCCTTCTATCTGGGCCGCCTG
                                                                 GAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #12148
                                                                                                                                                                                                   1334
                                                                                                                                                                                                                Claim 1; SEQ ID No 12148; 103pp; English.
                                                                                                                                                                                                   AGTITIGCCTTIGGGCAGCCTGACAACCACGGG
                                                                                                                                                                                                                                                                                                                AAS76344 standard; cDNA; 1519
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2000US-0649167
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P-PSDB; ABG12157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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23-AUG-2000;
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                                                                                                                                                                                                                      665
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                                                                                                                                                               546 GCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGTGGGGCCACCTCAAGCCAGCTG 605
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                        610 TACTCCCCCAGAGGCAACTGGGAGGTCAACGGGAAGACAATCGTCCCCTATAAGAAGGGT
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                                                                                            Length 1519;
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                                                                                                                      3; Indels
                                                                  Sequence 1519 BP; 297 A; 462 C; 489 G; 271 T; 0 other;
                                                                                                         3.4e-236;
                                                                                          Score 562; DB 23;
Pred. No. 3.4e-236;
                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                      0; Mismatches
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                                                                                                        Best Local Similarity 99.6%;
Matches 712; Conservative
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1084 ACAGA 1088

481 ACAGA 485

Db

ABN72904 standard; DNA; 690 BP

RESULT 13 **ABN72904** ABN72904;

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                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12557 tepresent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                         Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964 TCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACAAGGTGCATTTTCCCTTCCACA 1023
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                                                                                                                                                                                                                                                        Algate PA, Frudakis TN;
                                                                                                                                                                                                                                                                                                                                                           cancer, preferably ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 177; 299pp; English
                                                                                                                                                  98US-0216003.
99US-0338933.
99US-0404879.
                                                                                                 99WO-US30270
                                                                                                                                   98US-0215681
                                                                                                                                                                                                                                                        Mitcham JL, King GE,
                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                         WPI; 2000-431589/37
                              WO200036107-A2
 Homo sapiens
                                                                                                 17-DEC-1999;
                                                                                                                                                                                      24-SEP-1999;
                                                                                                                                   17-DEC-1998;
                                                                                                                                                   17-DEC-1998;
23-JUN-1999;
                                                                22-JUN-2000
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Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGAC 240
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Hill P, Albone E;
                                                                                                     Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.9%; Score 485; DB 24; Length 690; Best Local Similarity 100.0%; Pred. No. 1.9e-202; Matches 485; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 690 BP; 148 A; 197 C; 212 G; 131 T; 2 other;
                                                                  Ovarian carcinoma antigen polynucleotide #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 296; 408pp; English
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D,
                                                                                                                                                                                                                                                                                                                                                                                                                            Algate 1
Carter 1
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2000US-0667857.
2001US-0827271.
                                                                                                                                                                                                                                              17-JUL-2001; 2001WO-US22635.
                                                                                                                                                                                                                                                                                 2000US-0617747
                                                                                                                                                                                                                                                                                                                                                     18-JUN-2001; 2001US-0884441
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            , King GE,
Vedvick TS,
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                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                           WO200206317-A2
                                                                                                                                                                                                                                                                                                  10-AUG-2000;
20-SEP-2000;
04-APR-2001;
                                                                                                                                          Homo sapiens
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                                 02-JUL-2002
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Protease and associated protein-9; PPRG-9; anti-PPRG antibody; diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis; arteriosclerosis; atherosclerosis; burstlis; hepatitis; immune disorder; AIDS; Addison's disease; adult respiratory distress syndrome; allergy; hepatotoropic; antiinflammatory; virucide; antiarteriosclerotic; antiinflammatory; virucide; antipsoriatic; anti-HIV; antiallergic; immunosuppressive; antidiabetic; antianaemic; neuroprotective; human; ss.
                                                                                             TCTGTGACATCGGCTACGGGGGGGGGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA 1023
                                                                                                                                           1024 CCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTATT 1083
                                                  963
                                                                                                                   361 TCTGTGACATCGGCTACGGGGGGGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACA 420
                                                                                                                                                         GTCTCAACATCAGCACCTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGCC
                                              AAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCG
                                                          Bandman O, Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;
Corley NC, Yue H, Tang YT, Reddy R, Patterson C, Au-Young J;
                                                                                                                                                                                                                                                                                                                                                    Human Protease and associated protein-9 (PPRG-9) encoding cDNA.
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/bound_moiety= "Probe or Primer"
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326..370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human PPRG-9"
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233..310
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P-PSDB; AAY70015.
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11-FEB-1999;
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derived from KIDNTUTO CONA library. It encodes human protease and associated protein 9 (PPRG-9), which is expressed in urologic and musculoskeletal tissues. Anti-PPRG antibodies can be used as therapeutic antagonists, reagents for diagnosis and monitoring diseases and for isolating PPRG. PPRG nucleotide sequence can be used as probe or primer for diagnosis and monitoring of PPRG-related diseases and gene mapping. PPRG can be used in the treatment of call proliferative disorders like cancer, arteriosclerosis, atherosclerosis, bursitis, cirrhosis and hepatitis, and immune disorders like AIDS, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis and amyloidosis.
            New human proteases, useful for diagnosis, treatment and prevention of cell proliferative disorders such as atherosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                        The present sequence is a cDNA identified in Incyte clone 998626
                                                                                                                                                                                                                                                                                                                                                                                                24.9%; Score 467; DB 21; Length 855; 99.5%; Pred. No. 1.4e-194; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                     Sequence 855 BP; 152 A; 283 C; 257 G; 162 T; 1 other;
                                                          Claim 9; Page 105; 114pp; English.
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Matches 617; Conservative
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(HYSE-) HYSEQ INC.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from NIPO
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                                                                                      DNA encoding novel human diagnostic protein #17013.
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100.0%; Pred. No. 2.5e-164;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167.
                                              (first entry)
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The compinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                              1009 ATTITCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGTGTGTTCAG 1068
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358 GCCAGAACCAIGGACGICICAACAICAGCACCIGCCACIGCCACTGICCCCTGGCIACA 299
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                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                       GGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCCGGAGCCCTGAACAG
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amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                               Length 1934;
                                                                                                                     Indels
                                                                    Sequence 1934 BP; 409 A; 577 C; 576 G; 372 T; 0 other;
                                                                                             Score 388; DB 23;
Pred. No. 5.5e-160;
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98.8%;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polyucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or guantitating a polypeptide in tissue, as molecular weight markers and as for supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and can diagnostic coding sequences of the invention.

Conditional coding sequences of the invention.

Conditional coding sequences of the invention of mutations of specification, but was obtained in electronic format directly from WIPO are the coding sequences.
CTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAG 1036
                       1035 CTACGGGGGGAGCCCAGTGTGCCACCAATGTGCATTTCCCTTCCACCGGGGACCTGAGCTGAG 1094
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                                                                                1037 GATCGACGGAGACTGCTTCATGGTGTCTTCA 1067
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23-AUG-2000; 2000US-0649167
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977
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Sequence 906 BP; 175 A; 294 C; 286 G; 151 T; 0 other;

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Nishikawa T, Isogai T, Hayashi K,
Claim 1; Page 420; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK91830 standard; cDNA; 512
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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                                                                                                                                                                                                                                                                                                                                                                                                  419 A 419
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                                                                                            318 CCCTGCGGCTGACATGCGGAGGCTGGACTGGACAGCCTGGCCCAACTGGCTCAAGC 377
                                                                                  GTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCATGCTGCATCC 133
                                                                                                                      AGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTGGCACCAC 193
                                                                                                                                                          CIGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of diseases, diagnostics, raising
                              Gaps
                                                                Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition; ss.
                                              CAGGAAGGAGAGTTTCTTGCTCCTCCTCCTGCACACCGCCTGCGCAGCTGGGTCCAGCC
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          Length 906;
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                                                                                                                                                                                                                                                                                                                                                                                           Human EST-derived coding sequence SEQ ID NO: 326.
                                                                                                                                                                                                                                                                               378 CAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGC 416
                                                                                                                                                                                                                                                                      CAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGC 412
         Score 348; DB 23;
Pred. No. 1.9e-142;
0; Mismatches 1;
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-081451
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                    AAH98469 standard; cDNA; 517
          18.68;
99.78;
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antibodies and research use
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                             Matches 398; Conservative
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P-PSDB; AAM23810.
                   Similarity
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           Query Match
Best Local 3
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proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
The present invention provides the protein and coding sequences of novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238
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                                                                                                                                                                                                                                                             Sequence 517 BP; 89 A; 180 C; 159 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                    Query Match 11.1%; Score 208; DB 22;
Best Local Similarity 99.2%; Pred. No. 4.2e-81;
Matches 358; Conservative 0; Mismatches 3;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length molecules have been determined. Primers for synthesising the full length the CDNA are useful for clarifying the function of the protein encoded by the CDNA are useful for clarifying the function of the protein encoded by length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EDPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 ACAGGAAGGAGTTTCTTGCTCCTCCTGCACAACCGCCTGCGCAGCTGGGTCCAGC 312
                                                                  Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 CCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCCCTGA 252
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                 Claim 2; SEQ ID NO 290; 1380pp + sequence listing; English.
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     Kojima S, Otsuki T,
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 512 BP; 94 A; 166 C; 167 G; 82 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 201; DB 22;
Pred. No. 4.9e-78;
0; Mismatches 0;
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10.7%; Score 201; DB
Best Local Similarity 100.0%; Pred. No. 4.9,
Matches 201; Conservative 0; Mismatches
   Nagai K,
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                                                                                    use in genetic manipulation -
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 Sugiyama T,
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                                  WPI; 2001-524255/58
 Wakamatsu A,
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11-JAN-2000;
02-MAY-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                             830\ \mathrm{Primers} useful for synthesizing full length cDNA clones and their use in genetic manipulation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 ACAGGAAGGAGATTTCTTGCTCCTCTCCCGCAAACGGCCTGCGCAGCTGGGTCCAGC
                                                                                               Example 11; SEQ ID NO 1693; 1380pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #17014.
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100.0%; Pred. No. 4.9e-78;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
             WPI; 2001-524255/58
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypurclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in the constant of a sesses blodiversity and and and constant of the traits to assess budgiversity and and and application of mutations of the constant of the constan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 AGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTC 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            737 GCTCTGCACAGAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGAACCATGCAGGGGGGGCTCTG 796
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                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #24309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 122; DB 23;
Pred. No. 1.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prea. ...
                                                                                                                                                                                                             Claim 1; SEQ ID No 17014; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS88505 standard; cDNA; 3660 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .58:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-0540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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  WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                            P-PSDB; ABG17023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantifathing a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and the protein expression or sesses biodiversity and the protein expression or sesses biodiversity and the protein expression or sesses biodiversity and the protein expression of mutations and the protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1236 GGCTCACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGGC 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2935 GGGCTCACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGAGCACCAGGCC 2994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; DB 23; Length sove
Pred, No. 2.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #25046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2995 TICACCAGTTTTGCCTTTGGGCAGCCTGACACCAGGG 3033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 24309; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS89242 standard; cDNA; 3660 BP
                                                                                     Tang YT;
23-AUG-2000; 2000US-0649167.
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                                                                                                                             WPI; 2001-639362/73
                                                                                   Liu C,
                                         (HYSE-) HYSEQ INC
                                                                                                                                                 P-PSDB; ABG24318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                                                                                                                                                                                                        biodiversity
                                                                                   Drmanac RT,
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30-MAR-2001; 2001WO:US08631.

Tang YT;

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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              30-MAR-2001; 2001WO-US08631.
                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                    WPI; 2001-639362/73.
                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                    P-PSDB; ABG17020
                                                                                                                                                                                                                                                                          biodiversity
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymedeptides are also used in diagnostics as expressed sequence tags polymediating expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving anomalizating antibodies against it, detecting or quantitating a polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing or binding partners are useful in medical imaginestics, forensics, gene mapping, identification of mutations of the produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human conditional put was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #17011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 5.3%; Score 99; DB 23; I Local Similarity 100.0%; Pred. No. 2.1e-33; es 99; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 25046; 103pp; English.
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                                                                                                    Tang YT
                31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
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                                                                                                                                      WPI; 2001-639362/73.
                                                                                                    Drmanac RT, Liu C,
                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                        P-PSDB; ABG25055
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags confidentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical magning of sites expressing (II). (I) and (II) are useful for treating isone supplement. (II) and its binding partners are useful in medical magning of sites expressing (II). (I) and (II) are useful for treating isone applications in the protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention.

Some and to produce other types of the invention.

Some and to produce data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO tree is the printed or specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1104 CAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCC 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 CAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 5.2%; Score 97; DB 23; Length 480
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
Matches 97; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1164 TTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 TTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGA 156
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11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9e-31;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #8941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 168 BP; 41 A; 45 C; 56 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%; Pred. No. 3.5
Matches 94; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 27593; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS73137 standard; cDNA; 1239 BP
                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.0%;
                                                   30-MAR-2001; 2001WO-US08631
                                                                                     31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                   WPI; 2001-639362/73
                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                    P-PSDB; ABG27602
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                                                                                                                                                                                                                                                                                                                             biodiversity
                 11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 26
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The invention relates to isolated polynucleotide (I) and . polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the printed and produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human and again of the sequences of the invention.

Specification but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1239 BP; 281 A; 298 C; 360 G; 300 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #12149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1420 GCAAAACCCGAAACCGTTACATCTGCCAGTTTGC 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 8941; 103pp; English.
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                                                                                                                                                          30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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WO200175067-A2.
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                          31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 GCAACGCCAC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 GCAACGCCAC 82
                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                         P-PSDB; ABG24318
                                                                         WO200175067-A2
                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              biodiversity
                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving. (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capposition for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human and approach of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 TCCGGCCTGTGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGCGGGCTTG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 792 BP; 176 A; 226 C; 239 G; 151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #24309.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%; Pred. No. 1.1.
Matches 86; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 12149; 103pp; English.
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100.0%; Pred. No.
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                                                                                                                                                                                                Tang YT;
                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                           31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                        WPI; 2001-639362/73.
                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                        P-PSDB; ABG12158
                                       WO200175067-A2.
              Homo sapiens.
                                                                                                                                                                                                                                                                                                            biodiversity
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                                                                   11-0CT-2001
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymeratase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags of orientifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forgeneic, disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human cream of an expension of the invention.

Note: The sequence data for this patent did not appear in the printed sequences the fire invention of mutations are fitp. wipo. int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 CCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCCTTTGTTGAAG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 CCCTGCAAGTGGGCTGGAACATGCAGCTGCCCGCGGGGCTTGGCGTCCTTTGTTGAAG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 99.2%; Pred. No. 1.2e-
                                                                                                                                                                                                                     Claim 1; SEQ ID No 24309; 103pp; English.
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RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 cccrecaagregecrecaacarecaecrecrecceceeegecrreccrrrrrrraag 152
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                                                                             Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3660 BP; 901 A; 903 C; 1053 G; 803 T; 0 other;
                                                   ONA encoding novel human diagnostic protein #25046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.2%; Score 79; DB 23;
nilarity 99.2%; Pred. No. 1.2e-24;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                          13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABG25055
                                                                                                                                                    WO200175067-A2.
                                                                                                                           Homo sapiens.
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                                                                                                                                                                             11-0CT-2001
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. A8564197-A8594564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 GACTCCTTCCGCTGGGCCACAGGGGAGCACCAGCCTTCACCAGTTTTGCCTTTGGGCAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.8%; Score 72; DB 23; Length 915; 100.0%; Pred. No. 1.5e-21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 915 BP; 212 A; 244 C; 264 G; 195 T; 0 other;
                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #17010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 17010; 103pp; English.
                              AAS81206 standard; cDNA; 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                             13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2001.
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                                                                                                               AAS81206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
AAS81206
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1320 CCTGACAACCAC 1331

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1 GCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTC 45

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The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have activities, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, and printers. They can be used in a range of diseases and design of probes that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses. The present sequence represents a probe used in an example from the present
                                                                                                                                                                                                                                                                                                                            Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding PRO secreted and transmembrane proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45 BP; 8 A; 17 C; 14 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Page 57; 123pp; English.
                                                                                                                                    AAX80091 standard; DNA; 45 BP.
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97US-0069278.
97US-0069334.
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97US-0069425.
97US-0069694.
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97US-0069702.
97US-0069870.
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97US-0068017.
98US-0070440.
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                                                                                                                                                                                                                                 (first entry)
                   178 CCTGACAACCAC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-371118/31.
                                                                                                                                                                                                                                                                                Human PRO347 probe
Homo sapiens.
                                                                                                                                                                                                                                 12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09928462-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                   AAX80091;
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                                                                                                              AAX80091
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PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO715; PRO115; PRO1112; PRO509; PRO853; PRO882; tumour cell; probe; tumourigenesis; cancer; neoplastic cell growth; cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a probe used to screen for cDNA encoding a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO2025, PRO217, PRO1025, PRO344, PRO344, PRO347, PRO357, PRO115, PRO1011, PRO1011, PROS03 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are laplieved to contribute to tumourigenesis. The polypeptides are useful target for the jecunification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                     Probe used to screen for cDNA encoding novel polypeptide PR0347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
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100.0%; Pred. No. 1.2
Live 0; Mismatches
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                            AAA46921 standard; cDNA; 45 BP
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99WO-US28409.
99WO-US28301.
99WO-US28565.
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99WO-US21090.
                                                                                                                                                                                                                                                                                                            99WO-US30095
                                                                                                                                                                                                                                                                                                                                        98US-0113296
                                                                                        03-OCT-2000 (first entry)
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Best Local Similarity 100.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botstein D, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                              WO200037640-A2.
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                           16-DEC-1999;
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30-NOV-1999;
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01-DEC-1999;
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                                                                                                                                                                                                                                                                            29-JUN-2000
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                                                             AAA46921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
RESULT 32
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                AAA4692
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Gaps

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1254 GCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTC 1298

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100.08; Preq. ... 2.4%; Score 45; 100.0%; Pred. No.

Best Local Similarity 100.

Query Match

Length 45; 0; Indels

DB 20; L

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haematopoiesis; clotting; kidney failure; wound healing; cancer; neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Eaton DL, Ferrara N, Filvaroff E;
, Godowski PJ, Grimaldi CJ, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                PRO: membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO341; PRO343; PRO343; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; ss.
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Pred. No. 1.2e-09;
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                                                                      Probe for cDNA encoding human PRO347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer #1 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 11; Page 103; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     Eaton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD33532 standard; DNA; 30 BP
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                                                                                                                                                                                                                                                                                                           98WO-US25108.
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98US-0113296.
                                                                                                                                                                                                                                                                            99WO-US28301
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                                        25-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillan KJ, Kljavin IJ,
                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                       Botstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  described (AAA49497).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and diagnostic agents
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                                                                                                                                                                                                               WO200032776-A2.
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Gerritsen ME,
                                                                                                                                                                                                                                                                            01-DEC-1999;
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                                                                                                                                                                                    Synthetic.
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              AAA49497;
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The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-175), human T175 or murine WDMM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability to the invention has the ability to modulate cell-cell interactions, heamatopoiesis and the ability to modulate colotting. Polypeptide and other uses. Polypeptide clotting. Polypeptide and other accesses a cell-cell interaction or activity. The collynucleotide of the invention aberrant expression or activity. The antibodies are useful for treating and for treating and treating cancer, TANGO-139 is useful in wound healing and for treating cancer, TANGO-110 (TANGO-125) useful in wound healing and for treating cancer, TANGO-110 is useful for treating neoplasia. TANGO-177 or WDMM-2 is useful for treating neoplasia. TANGO-177 or WDMM-2 is useful for treating cancer, are useful to treat pancreatic disorders, such as ischaemic heart disease, cardiovascular disease, and tumours, and influxy or trauma to the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g., creating experientials). TANGO-125, 110 and 175 molecules are useful to treat chick disorders, such as inflammatory disorders. TANGO-175, or disease and tumours. And plower and experience of sorders, such as inflammatory disorders. TANGO-175, or disease and tumours. TANGO-139, 125, 110, and 175 molecules are useful for treating proliferative disorders, inflammatory disorders. TANGO-175, or wDNM-2 activity also include apoptotic disorders, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mallitus, immune-related disorders, inflammatory disorders, viral immune-related disorders, e.g., immune-related disorders, e.g., immune-related disorders, e.g., inmunoedicitic acids of the invention disorders. The plant apoptotic disorders and apoptotic disorders. The nucleic acids of the invention
heart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive; glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; hemostatic; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic; cytostatic; nephrotropic; antidiabelic; cerebroprotective; tranquilliser; hypotensive; tunnur; injury; trauma; antianginal; vasotropic; antiuloer; hepatotropic; antipsoriatic; antiallergic; dermatological; virucide; pCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodearl ADJ, Mccarthy SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 53; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0065661.
98US-0102705.
98US-0124538.
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2001; 2001US-0790264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0065363.
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99US-0337930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOLT/) HOLTZMAN D A.
(GOOD/) GOODEARL A D J.
(MCCA/) MCCARTHY S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-303420/34.
                                                                                                                                                                                                                                                                                                                                             JS2002028508-A1.
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                                                                                                                                                                                                                                                                                                 Jnidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998;
22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1998;
23-APR-1999;
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 are used in gene therapy. The present sequence is a PCR primer used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody against proteins expressed in neoplastic cells, useful for
                                                                                                          ó:
                                                                                                                                                                                                                                                                                                                                                PRO347; cancer; tumour; diagnosis; therapy; human; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney AL, Hillan KJ, Lawrence DA;
                                                                      Query Match 1.6%; Score 30; DB 24; Length 30; Best Local Similarity 100.0%; Pred. No. 0.0047; Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predictors of the prognosis of tumour treatment.
                                       Sequence 30 BP; 3 A; 8 C; 11 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;
                                                                                                                            108 GGGCCCAACAGACCCATGCTGCATCCAGAG 137
                                                                                                                                             30 GGGCCCAACAGACCCATGCTGCATCCAGAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 54; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0109304.
98US-0070440.
98US-0083500.
98US-0086414.
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                                                                                                                                                                                                                                 AAX87290 standard; DNA; 27
                                                                                                                                                                                                                                                                                        27-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                     PRO347 probe 44176.tm.pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-430385/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botstein D, Godda
Roy MA, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998;
10-JUN-1998;
10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9935170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-1999;
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29-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                    RESULT 35
AAX87290/c
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PCR primers AAA46957-58 and probe AAA46959 were used to isolate cDNA encoding a novel human polypeptide. The specification describes novel polypeptides designated PR0201, PR0292, PR0327, PR01265, PR0344, PR0343, PR0347, PR0357, PR01017, PR01112, PR0569, PR0569, PR0344, PR0343, These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The POLYPEPTIGES are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment diagnosis of neoplastic cell growth and proliferation in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New anti-polypeptide antibody useful in the treatment and diagnosis of
                                                                                                                                                  PRO201; PRO392; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; probe; tumourigenesis; cancer; neoplastic cell growth; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                       PCR primer used to amplify cDNA encoding novel polypeptide PRO347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 27; DB 21; Length 27; 100.0%; Pred. No. 0.098; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neoplastic cell growth and proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1714 IGGGAAGATGGGCTTCAATTAGATGGC 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Page 110; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 TGGGAAGATGGGCTTCAATTAGATGGC 1
                              AAA46958 standard; cDNA; 27
                                                                                                                                                                                                                                                                                                                                                                                   99WO-US12252.
99WO-US20111.
                                                                                                                                                                                                                                                                                                                           99WO-US30095.
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                                                                                        03-OCT-2000 (first entry)
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Best Local Similarity 100.0°
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
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                                                                                                                                                                                                 PCR primer; ss.
                                                                                                                                                                                                                                                              WO200037640-A2.
                                                                                                                                                                                                                                 Homo sapiens.
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30-NOV-1999;
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01-DEC-1999;
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                                                                                                                                                                                                                                                                                           29-JUN-2000
                                                              AAA46958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI;
                 AAA46958/c
RESULT 36
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AAA49533/c RESULT 37

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Gaps

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1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740

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The present invention describes nucleic acids encoding PRO secreted and
secreted protein; transmembrane protein; inflammation disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. -. +ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Page 57; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1777 CTCTCTTCCACCTGGCCCAGACCC 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX80089 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0069694.
97US-0069696.
97US-0069702.
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97US-0069873.
97US-0068017.
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97US-0067411.
97US-0069278.
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                                                                                                                                                                                                                                                                            98WO-US25108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                               PCR primer; ss.
                                                                                                                Homo sapiens.
                                                                                                                                                                 W09928462-A2
                                                                                                                                                                                                                                                                            01-DEC-1998;
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2-DEC-1997;
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                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX80089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuan J;
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OOSXXE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides which are designated as PRO polypeptides are described. The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources. Two primers (AAA49532, AAA49534) were used for gene amplification analysis of the sequence encoding human PRO347. A hybridisation probe also used in the analysis is described (AAA49533).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eaton DL, Ferrara N, Filvaroff E;
A, Godowski PJ, Grimaldi CJ, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                     PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO415; PRO415; PRO415; PRO325; PRO525; PRO515; PRO515; PRO515; PRO515; PRO515; PRO515; PRO516; PRO516;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 7 A; 10 C; 3 G; 7 T; 0 other;
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                                                                                                                                                                    Probe for analysing human PRO347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX80090 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUG-1999 (first entry)
  AAA49533 standard; DNA; 27
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botstein D, Ea
ME, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillan KJ, Kljavin IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                          WO200032776-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1999;
                                                                                                                25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX80090;
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                                                         AAA49533;
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           δλ
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transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. PRO protein having homology to complement proteins may be used in inflammatory responses. The present sequence represents a PCR primer used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 20; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 5 A; 3 C; 13 G; 3 T; 0 other;
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PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                     Wood WI;
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    δλ
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                                                                                                                                                                                                                                                                                                                                                       The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-iproliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses. The present sequence represents a PCR primer used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO201; PRO392; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer used to amplify cDNA encoding novel polypeptide PRO347.
                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding PRO secreted and transmembrane proteins
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                                                                                                                                                                                                                                                                          Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                          Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                       Example 11; Page 57; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1221 AGGAACTTCTGGATCGGGCTCACC 1244
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                                                                                                                                                                                                                                                                       Baker KP, Chen J, Goddard A,
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                                                                                                   980S-0075945.
970S-0067411.
970S-0069378.
970S-0069335.
970S-0069425.
970S-0069694.
970S-0069694.
970S-00696970.
970S-0069870.
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98US-0074086.
98US-0074092.
                                                                                   98WO-US25108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.3
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                    WPI; 1999-371118/31
PCR primer; ss.
                                                                                                                               11-DEC-1997;
11-DEC-1997;
12-DEC-1997;
                             Homo sapiens
                                             WO9928462-A2
                                                                                  01-DEC-1998;
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                                                              10-JUN-1999
                                                                                                                     11-DEC-1997
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                                                                                                              03-DEC-1997
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                                                                                                                                                                                                                           09-FEB-1998
                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             .nvention.
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New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primers AAA46919-20 were used to amplify cDNA encoding a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO322, PRO347, PRO343, PRO343, PRO341, PRO341, PRO357, PRO10112, PRO595, PRO345, PRO345, PRO91017, PRO1112, PRO509, PRO653 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodles agains these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer used to amplify cDNA encoding novel polypeptide PRO347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Page 101; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1221 AGGAACTTCTGGATCGGGCTCACC 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGGAACTTCTGGATCGGCTCACC 24
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                                                                                                                                                                                                                              98US-0113296.
99WO-US05028.
99WO-US12252.
99WO-US20111.
99WO-US21090.
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99WO-US28409
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99WO-US28565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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                                                     WO200037640-A2.
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
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                                                                                                                                                                                                                                                                                                02-JUN-1999;
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15-SEP-1999;
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                                                                                                                                                                                                                                    22-DEC-1998;
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98US-0113296
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                                                                                                                                                                                                                                                                                                                             Local Similarity
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22-DEC-1998;
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22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                     24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA49496;
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Qγ
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                                                                                                                                                                                                                                                                                                                                                  against
                                                                                                                                                                                                                     New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                        PCR primers AAA46919-20 were used to amplify cDNA encoding a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO322, PRO327, PRO344, PRO343, PRO343, PRO315, PRO115, PRO1101, PRO1112, PRO599, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies agains these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in mammals.
                                                                                                                                                                      Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO434; PRO431; PRO41; PRO4323; PRO599; PRO533; PRO514; PRO515; PRO515; PRO515; PRO516; Protein inhibition; Probe; Primer; SS.
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0
                                                                                                                                                                      Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA,
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.3%; Score 24; DB 21; Length 24; Best Local Similarity 100.0%; Pred. No. 2; Matches 24; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 5 A; 3 C; 13 G; 3 T; 0 other;
                                                                                                                                                                                                                                                      Example 9; Page 101; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1777 CTCTCTTCCACCTGGCCCAGACCC 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 CTCTTCCACCTGGCCCAGACCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA49495 standard; DNA; 24 BP
                                                                                            99WO-US28313.
99WO-US28409.
99WO-US28301.
                                                            99WO-US12252.
99WO-US20111.
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98US-0112850
                                                                                 99WO-US21090
                    99WO-US30095
                                         98US-0113296
                                                                                                                           99WO-US28565
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                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                  WPI; 2000-452188/39.
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16-DEC-1998;
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                    16-DEC-1999;
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                                                                                 15-SEP-1999;
                                                                                                      30-NOV-1999;
01-DEC-1999;
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29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                 Wood WI;
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AAA49495
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New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic agents
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Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
                                                                        Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%; Score 24; DB 21; Length 24; 100.0%; Pred. No. 2; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer for isolating cDNA clones encoding human PRO347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page 103; 187pp; English.
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98US-0112850.
98US-0113296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               described (AAA49497).
                                                                                                                                                                                                                                  WPI; 2000-412324/35.
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                                                                                                          polypeptides which are designated as PRO polypeptides are described the membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources. Two primers (AAA49495, AAA49496) were used to isolate the cDNA sequence encoding human PRO347. A hybridisation probe for human PRO347 is also
           New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYP2A6v2; cytochrome P450 isoenzyme; drug metabolism; gene therapy; polymorphism; genotyping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytochrome P450 isoenzyme mutant genes - used for developing prods. for detecting or treating sensitivity to drugs or carcinogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
"base n at position 2019 is not identified
in the specification"
                                                                                                                                                                                                                                                                                                                               ·.
                                                                                              New human nucleic acids encoding secreted and transmembrane
                                                                                                                                                                                                                                                                                                1.3%; Score 24; DB 21; Length 24; L00.0%; Pred. No. 2; Ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytochrome P450 isoenzyme mutant CYP2A6v2 genomic DNA.
                                                                                                                                                                                                                                                                     Sequence 24 BP; 5 A; 3 C; 13 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                 Example 11; Page 103; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     1777 CTCTTCCACCTGGCCCAGACCC 1800
                                                                                                                                                                                                                                                                                                 1.50,
100.0%; PIE
                                                                                                                                                                                                                                                                                                                                                                     24 CTCTCTTCCACCTGGCCCAGACCC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 12; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT12249 standard; DNA; 7216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95GB-0007640.
94GB-0012054.
95GB-0002728.
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                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
/note=
                                      and diagnostic agents
                                                                                                                                                                                                                                         described (AAA49497).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-049706/05.
                                                                                                                                                                                                                                                                                                             Local Similarity
es 24; Conserv
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misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9534679-A2
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13-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-APR-1996
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                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                            Matches
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cDNA (AAT12248) and genomic (AAT12249) sequences were detected for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
a new mutant variant, designated CYP2A6v2, of cytochrome P450 isoenzyme CYP2A6, an allele associated with drug sensitivity and carcinogen metabolism. Alterations in sequence from the wild-type CYP2A6 gene occur within exons 3, 6 and 8, and are attributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatorid arthritis; glomerulonephritis; asthma: thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                            gene conversion. The nucleic acid sequences can be used to determine a patient's sensitivity to drugs or to chemical or environmental carcinogens, and can also be used in gene therapy, in gene polymorphism detection and in genotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA differentially expressed in granulocytic cells #837.
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                                                                                                                                                                                                                                                                                                                                                                                                           / Match 1.1%; Score 21; DB 17; Length 7216; Local Similarity 100.0%; Pred. No. 30; Conservative 0; Mismatches 0; Indels of the second of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                               Sequence 7216 BP; 1646 A; 2195 C; 1747 G; 1627 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 837; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK84266 standard; cDNA; 8778 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1605 GGCAGAGAGAGGCAGGGAGG 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2001; 2001WO-US30821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1634 GGGCAGAGAGAGGCAGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-435328/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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ID ABK8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 45
       8888888888888
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cc chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; the level of expression of the gene is indicative of inflammation; c. (4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having consterile inflammatory disease, by contacting a tissue having cinflammatory disease, by contacting a tissue having condulating ds. M3 is useful for detecting GN, MZ is useful for condulating ds. M3 is useful for screening an agent capable of modulating GN preferably in an inflammation in a tissue; M4 is useful for exportance in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, inflammatory disease (e.g. psoriasis, rheumatoid arthritis, gratic inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, or protozoal infection, viral infection, and M5 is expendit for treating one of the above conditions. The persent contractive colitis, rhe patent did not form part.

Conflammatory disease, crohn's disease, ulcerative colitis, esquence represents a gene differentially expressed in granulocytes. Conflammatory by the pathogen of the above conditions. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL; SNP; gene; neonatal pertussis; whooping cough; haplotyping; ds; single nucleotide polymorphism.
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/standard_name= "Single nucleotide polymorphism"
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replace (3444,C)
/*tag= b
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4067..23781
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                                                                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 21; DB 24; Length 8778;
100.0%; Pred. No. 29;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8778 BP; 2030 A; 2663 C; 2014 G; 2071 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replace (6682,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace (4260,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK12674 standard; DNA; 27780 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1492 GGCAGAGAGAGGCAGGGAGG 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1634 GGGCAGAGAGAGGCAGGGAGG 1654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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replace (6783,G)

variation

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence which is a polymorphic variant of a reference sequence for Selectin L Lymphocyte Adhesion Molecule I (SELL) gene. SELL polypeptide is useful for screening for drugs targeting the polypeptide. Oligonucleotides derived from (I) are used to target SELL and a haplotype or haplotype pair of SELL gene. These are useful in developing diagnostic tests and therapeutic treatments for neonatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel genetic variants of selectin L lymphocyte adhesion molecule 1 (SELL) gene useful for therapeutic purposes and for expressing SELL protein useful in identifying drugs to treat whooping cough .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "Single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kumar AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anastasio AE, Bieglecki KM, Kliem SE,
                                                                                                                                                                                                                                                                                                                                                                                                  replace (19155,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                           replace (23767,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace (24041,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace (24122,T)
                                                                                                                                                                                                                                                                        replace (13838,A)
                                                                                                                                                                                                                                                                                                                replace (18851,G)
                                                                                                                                                                                                                                                                                                                                                           replace (19074,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace (23925,C)
                                                                                                                                                                                                                                replace (12363,A)
                                                                                                                                                                                       replace (10868,T)
                     replace (6784,T)
/*tag= h
                                                                                                       replace (7027,C)
                                                                                                                                                replace (8220,C)
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                                                                replace (6997,C)
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P-PSDB; AAU76539.
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pertussis (whooping cough). (I) is useful for studying the expression and function of SELL and expressing SELL protein for use in screening for candidate drugs to treat diseases related to SELL activity. The polymorphism and haplotype data are useful for validather whether SELL is cut ugs and reducing bias in clinical trials of such drugs. Establishing in cut sell and reducing bias in clinical trials of such drugs. Establishing improving the efficiency and reliability of several steps in the cit siscovery and development of drugs for treating diseases associated with SELL activity e.g. neonatal pertussis (whooping cough). The haplotyping cough is useful to validate SELL as candidate target for treating a sectivity. The method is also useful in screening for compounds.

CC SELL activity as a specific condition or disease predicted to be associated with SELL to treat a specific condition or disease predicted to be associated with SELL to treat a specific condition or disease predicted to be associated with SELL to treat a specific condition or disease predicted to be associated with SELL activity. For an applotype pairs present in individual members of a ctivity for each of the most frequent SELL is useful in studying to compounds that display the highest desired agonist or antagonist condition. A polymorphic variant of SELL is useful in studying the effect of the variation on the biological activity of SELL, on the freatment of neonated pertussis (whooping cough) and in assays to measure the condition of more candidate drugs targeting the SELL condition the present sequence represents the SELL gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human adenosine receptor related polynucleotide SEQ ID NO:2480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 21; DB 24; Length 27780;
100.0%; Pred. No. 27;
ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27780 BP; 8061 A; 5257 C; 5581 G; 8860 T; 21 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA34791 standard; DNA; 138169 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 12949 GCAGAGAGGCAGGGAGGCC 12969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0%; P. Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1636 GCAGAGAGGCAGGGAGGCC 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US17712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0095212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200009525-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1999;
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    δλ
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New antisense oligonucleotides useful for treating e.g. pulmonary

(UYEC-) UNIV EAST CAROLINA.

WPI; 2000-205971/18.

Nyce JW;

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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 158), which cargets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, andiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating conflictions, pulmonary vasoconstriction, allergies, pulmonary hypertension, emphysema, chronic obstructive asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive carcinomas, and cancers which may metastasise to the lungs, including the presset defects. The A-containing ONs break down with the crease of deoxyadenosine which activates adenosine content of crease of deoxyadenosine which activates adenosine content of the obstactic sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO: 1 to 185, but the sequences of differ from the previously named sequences. SEQ ID NO: 1 to 185, but the sequences of invention No. B. Sequences given in the disclosure of the present invention Analy3233 to Analy3233 to Analy3233 to Analy3233 to Analy3233 to Analy323 to the previously named sequences. SEQ ID NO: 1 to 185, invention to not match up with their corresponding SEQ ID NO: sequences are also called sequences of the previously named sequences of the previously named sequences. SEQ ID NO: 1 to 185, and then the previously named sequences of the previous of the previous of invention do not match up with their corresponding SEQ ID NO: sequences are also called sequences of the previous sequences are also called sequences o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 138169 BP; 41766 A; 28262 C; 26273 G; 41868 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 21; DB 21; Length 138169;
100.0%; Pred. No. 25;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ELAM-1 polynucleotide fragment #2480.
                                                                                                        Disclosure; Page 613-645; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF20913 standard; DNA; 141589 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 31241 GCAGAGAGGCAGGGAGGCC 31221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.C
Matches 21, Conservative
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                                                        cancers
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chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors. CNS and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system receptors, defensins, growth factors, vascactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (specially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasconstriction, inflammation, condition selected from pulmonary vasconstriction, inflammation, hypertension, emphysema, chronic obstructive pulmonary distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary phyprotections, pulmonary infections, bronchitis, and/or cancer. AARI8434 to AARI8433 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Low adenosine antisense oligonucleotide; phosphorothicate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antihilammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                oligonucleotides and compositions (1) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (1) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiathmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and binding proteins, adhesion molecules and their receptors, cytokine and
                                                                                                                                                                                                Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human low adenosine antisense oligonucleotide related sequence #2694.
                                                                                                                                                                                                                                                                                                                                                                present invention describes low adenosine (A) content antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 141589 BP; 42856 A; 28938 C; 26863 G; 42932 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 21; DB 21; Length 141589;
100.0%; Pred. No. 25;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                Disclosure; Page 178-205; 1592pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF21127 standard; DNA; 141589 BP
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                (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                      WPI; 2000-679539/66.
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                                                                                                       Nyce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF21127/c
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with capturing peptide factors and malignancies, such as stimulating and certivating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, central nervous and non-nervous system creeptors, defensins, and peripheral nervous and non-nervous system creeptors, defensins, arowth factors, vasoactive peptides and respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergies, asthma, impeded respiratory millering respiratory obstruction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiratory pulminary respiratory of the spiratory respiratory is allergies, asthma, impeded respiratory respiratory is allergies, asthma, impeded respiratory respiratory is allergies, asthma, impeded respiratory constriction, inflammation, allergies, asthma, impeded respiratory constriction will allergies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
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0
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 992-1024; 1592pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF21152 standard; DNA; 141589 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy 1636 GCAGAGAGAGGCAGGGAGGCC 1656
                                                                                                                                                                                                                                                       990S-0127958.
                                                                                                                                                                                                          24-MAR-2000; 2000WO-US08020.
                                                                                                                                                                                                                                                                                                  (UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-679539/66.
                                                                                                                                                                                                                                                                                                                          (NYCE/) NYCE J W.
                                                                                                                    WO200062736-A2.
                                                                         Homo sapiens
                                                                                                                                                                                                                                                       06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                  26-OCT-2000.
                                 cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF21152;
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Gaps

pulmonary hypertension; emphysema; pulmonary transplantation rejection;

14-MAR-2001

(first entry)

Human low adenosine antisense oligonucleotide related sequence #2719.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antlinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; pulmonary obstruction; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

cancer; ss.

WO200062736-A2. Homo sapiens.

26-OCT-2000.

24-MAR-2000; 2000WO-US08020.

99US-0127958. 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Disclosure; Page 1049-1081; 1592pp; English.

the animonal controlled and the controlled with a cartivating obtains and or activity of target polypeptides associated with a cartivating peptide factors and maignancies, such as stimulating and cartivating peptide factors and maignancies, such as stimulating and cartivating peptide factors and maignancies, transcription factors, chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradkinin receptors, cytokine and nervous system (CNS) and peripheral nervous and non-nervous system creeptors, defensins, growth factors, vascative peptides and ransmitters, defensins, growth factors, vascative peptides and creeptors, binding proteins and mallingancy associated proteins. The creeptors, binding proteins and mallingancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders and/or bronchoconstriction (especially pulmonary obstruction (especially pulmonary obstruction cand/or surfactant hypoproduction which are associated with a disease or and/or surfactant hypoproduction which are associated with a disease or condition selected fine pulmonary vascoonstriction, inflammation, allergy (es) pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary condition, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, creamons, invention condition antisense oligonucleotides used in the exemplification of the present invention. The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the the present invention.

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Sequence 321, Application US/09404879A

Patent No. 6468546

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Midcham, Jennifer L.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER.
FILE REFERENCE: 210121.462C2
CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 690
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US-08-49-1596-5
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; OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 100.
Matches 485; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
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 FEATURE:
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100.0%; Pred. No. 3.5;
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DRUG
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07605
FILING DATE: 16-JUN-1995
ATTORNEY, AGENT UNPORMATION:
NAME: DOTOCHLY R. Auth
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4196PC
TELECOMMULICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7216 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: RAPPLICATION NUMBER: US/08/750.70? FILING DATE: CLASSIPTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GONZAIGZ, Frank J.; Id
TITLE OF INVENTION: DEFECTS IN DR
TITLE OF INVENTION: METABOLISM
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08750703
Patent No. 5891633
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CYP2A6v2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION:
US-08-750-703-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                     ACAGA 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                          ACAGA 485
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-750-703-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Sequence 1, Application US/08788750
; Sequence 1, Application US/08788750
; Patent No. 5910430
; GENERAL INFORMATION:
    APPLICANT: Ellis, Catherine
    APPLICANT: Bergsma, Derk
    TITLE OF INVENTION: No. 5910430el G-Protein Coupled Receptor
    TITLE OF INVENTION: (HTADX50)
    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 19; DB 4; Length 1329;
100.0%; Pred. No. 29;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,750
FILING DATE: 24-JAN-1997
CLASSTFICATION: 435
PRIOR APPLICATION: 435
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
EARLIER APPLICATION NUMBER: PCT/US98/04858 EARLIER FILING DATE: 1998-03-12 EARLIER APPLICATION NUMBER: 60/040,762
                                                               EARLIER APPLICATION NUMBER: 00/040,702
EARLIER FILING DATE: 1997-03-14
EARLIER PILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER PILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-19
NUMBER: 05 SEQ ID NOS: 118
SOFTWARE: PALEORITIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1140)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1645 GGCAGGGAGGCCAGTGAGG 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 GGCAGGGAGGCCAGTGAGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΡA
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US-08-788-750-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Post SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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1.1%; Score 21; DB 2; Length 8779;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               APPLICANT: Gonzalez, Frank J.; Idle, Jeffrey R. TITLE OF INVENTION: DEFECTS IN DRUG TITLE OF INVENTION: METABOLISM NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DOTOTHY R. AUTH
REGISTRATION NUMBER: 36.434
REFERENCE/DOCKET NUMBER: 2026-4196PCT
TELECOMNUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07605
FILING DATE: 16-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09152060 Patent No. 6448230\,
                                                                                                                                                         RESULT 3
US-08-750-703-4/c
; Sequence 4, Application US/08750703
; Patent No. 5891633
; GBNERAL INFORMATION:
APPLICANT: Gonzalez, Frank J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1493 GGGCAGAGAGGCAGGGAGG 1473
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                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Ave.
CITY: New York
                                                                  1605 GGGCAGAGAGGCAGGGAGG 1585
                                        1634 GGGCAGAGAGAGGCAGGGAGG 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 8779 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CYP2A13
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COTHER INFORMATION:
US-08-750-703-4
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US-09-152-060-25/C
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Gaps

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165 GCTGTGCTCCTGGCCCTCC 183
                          Ouery Match
Best Local Similarity 100.0
Matches 19; Conservative
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: New York
RY: U.S.A.
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Matches 19; Conserva
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-757-669A-19/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                       .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07960389
Patent No. 5705511
GENERAL INFORMATION:
APPLICANT: HAYASHIDA, Kasuhiro;
TITLE OF INVENTION: Human GM-CSF Receptor Component NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: System Software 7.1 SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/960,389 FILING DATE: 07-JAN-1993 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JAN-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 554,745
FILING DATE: 18-JUL-1990
APPLICATION NUMBER: PCT/US 91/04846
FILING DATE: 16-JUL-1991
ATTORNEY AGENT INFORMATION:
                                                                                     ATG50048
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATGS(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (908) 298-2902
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3475 base pairs
TYPE: nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                   1645 GGCAGGGAGGCCAGTGAGG 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disc
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System (
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.C
Matches 19; Conservative
                                                                                                                                        TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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US-07-960-389-1
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ADDRESSEE: COOPER & PINCEL STREET COOPER & PINCEL STREET.
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               DB 1; Length 3475; 28;
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                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
. 26;
                                  Pred. No. 28;
Mismatches
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                 Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                    US-08-770-379-19/c; Sequence 19, Application US/08770379; Patent No. 5849564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
GAPPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
1.0%; SCOL
100.0%; Pre
0;
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR EQU ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 31100 Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 523
TELECOMMUNICATION INFORMATION:
                                                                                                                   1563 GCTGTGCTCCTGGCCCTCC 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 13366 CTGCCATGGGGTTTGGCAA 13348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1351 CTGCCATGGGGTTTGGCAA 1369
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TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF

Moore, Patrick S.

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/329,704
FILING DATE: 436
CLASSIFICATION: 436
                                                                                                    Sequence 3, Application US/08329704

Patent No. 5786210

GENERAL INFORMATION:

APPLICANT: Kenner, Gregory S.

APPLICANT: Kennedy, Jacqueline L.

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: MAMMALIAN THYMOKINE GENES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNX Research Institute

STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICR APPLICATION 047A.

APPLICATION NUMBER: US 08/193,483
FILING DATE: 08-FEB-1994
PRICR APPLICATION DATE:
APPLICATION NUMBER: US 08/231,421
FILING DATE: 22-APR-1994
ATONNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/08472604
; Patent No. 5877285
; GENERAL INFORMATION:
APPLICANT: Kennedy, Jacqueline L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
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Best Local Similarity
Matches 18; Conserva
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US-08-329-704-3
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                                                                  RESULT 10
US-08-329-704-3
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APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Bohenzky, Roy A
APPLICANT: Edelman, Isidore S
APPLICANT: Edelman, Isidore S
APPLICANT: More, Patrick S
TITLE OF INVENTION: UNIQUE ASSCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: UNGER THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 26;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Score 19; DB 4; Length 35100; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/757,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                             ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09230371A Patent No. 6348586 GENERAL INFORMATION: APPLICANT: Chang, Yuan
                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 13366 CIGCCAFGGGGTFTGGCAA 13348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 35100 base pairs
TYPE: nucleic acid
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Best Local Similarity 100.
Matches 19; Conservative
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Matches 19; Conservative
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                   COUNTRY: U.S.A. ZIP: 10036
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                                 Gaps
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1.0%; Score 18; DB 1; Length 562;
100.0%; Pred. No. 84;
ive 0; Mismatches 0; Indels
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Query Match 1.0%; Score 18; DB 2; Length 562; Best Local Similarity 100.0%; Pred. No. 84; Matches 18; Conservative 0; Mismatches 0; Indels
     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible '
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,537
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kelner, Gregory S.
APPLICANT: Kennedy, Jacqueline L.
APPLICANT: 2lotnik, Albert
TITLE OF INVENTION: MAMMALIAN THYMOKINE GENES
ONNERER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,117
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA: 08 08/231,421
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/193,483
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P. 1900
REFERENCE/DOCKET NUMBER: DX0430K1GC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ. 1D NO: 3:
SEGURATION FOR SEQ. DI NO: 3:
TYPE: NUCLEIC CACIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15..356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LOCATION:
US-08-486-117-3
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100.0%; Pred. No. 84;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,604
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/472,604
FILING DATE: 07-JUN-1995
FILING APPLICATION NUMBER: US/08/329,704
FILING DATE: 25-OCT-1995
PRIOR APPLICATION NUMBER: US/08/329,704
FILING DATE: 25-OCT-1995
PRIOR APPLICATION NUMBER: US/08/231,421
FILING DATE: 22-APR-1994
PRIOR APPLICATION NUMBER: US/08/231,483
FILING APPLICATION NUMBER: US/08/193,483
FILING BATE: US/08/193,483
FILING BATE: US/08/193,483
FILING MATER: US/08/193,483
FILING BATE: US/08/193,483
FILING BATE: US/08/193,483
FILING BATE: US/08/193,483
FILING CALIDY EGWIN P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX/04/08/193,483
TELEFRAN: 415-485-1996
TELEFRAN: 415-485-1996
TELEFRAN: A15-485-1996
TATTELEFRAN: A15-485-1996
TATTELEFRAN: A15-485-1996
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APPLICANT: Kelner, Gregory S.
APPLICANT: Kenner, Jacqueline L.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN THYMOKINE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                TITLE OF INVENTION MAMMALIAN THYMOKINE GENES NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                     ADDRESSEE: DNAX Research Institute
STREET: 901 Callifornia Avenue
CITY: Palo Alto
STATE: Callifornia
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICANT: Zlotnik, Albert
                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 TCCTGGCCCTCCTTGGCA 189
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Best Local Similarity 100.C
Matches 18; Conservative
                                                                                                                                                                                                                             ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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                                                                                                                                                                                                             USA
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; LOCATION:
US-08-472-604-3
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COUNTRY:
ZIP: 9430
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-486-117-3
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EARLIER P
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EARLIER
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EARLIER
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100.0%; Pred. No. 84;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 186 HUMAN SECTECED PLOCED CORRENT APPLICATION NUMBER: US/09/149,476 CURRENT FILING DATE: 1998-09-08 EARLIER PELING DATE: 1998-03-08 EARLIER PELING DATE: 1998-03-06 EARLIER PILING DATE: 1998-03-06 EARLIER PILING DATE: 1997-03-07 EARLIER PILING DATE: 1997-05-23 EARLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,483
FILING DATE: 08-EEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching' Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0430K1GD
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 3:
APPLICATION NUMBER: US 08/329,704 FILING DATE: 25-0CT-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/231,421 FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 232, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.0%; Sur
Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 TCCTGGCCCTCCTTGGCA 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY: CDS
, LOCATION: 15..356
US-08-477-537-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-149-476-232
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EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
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R APPLICATION NUMBER: 60/047,613

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,582

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,596
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APPLICATION NUMBER: 60/056,662
FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
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EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER PAPLICATION NUMBER: 60/056,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
                                                         60/047,618
                                                                                   FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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EARLIER APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,601
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EARLIER APPLICATION NUMBER: 60/047,592
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EARLIER FILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,614
SR APPLICATION NUMBER: 60/043,578
R FILING DATE: 1997-04-11
R RAPLICATION NUMBER: 60/043,578
SR FILING DATE: 1997-04-11
SR RAPLICATION NUMBER: 60/043,576
SR FILING DATE: 1997-04-11
SR RAPPLICATION NUMBER: 60/047,501
SR RELING DATE: 1997-05-23
SR APPLICATION NUMBER: 60/047,501
SR FILING DATE: 1997-05-23
                                                        R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,637

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,903

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,888
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047,595
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,599
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R APPLICATION NUMBER: 60/047,588
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,586
R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,879
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,910
APPLICATION NUMBER: 60/056,872
                  FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,894
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APPLICATION NUMBER: 60/056,864
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,845
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APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,594
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
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APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,664
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
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APPLICATION NUMBER: 60/056,875
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APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Steleinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Burgess, Christopher C.
APPLICANT: Burgess, Christopher C.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Derfi, Adnan
APPLICANT: Derfi, Adnan
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
EENOTH: 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 18; DB 4; Length 629;
100.0%; Pred. No. 84;
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EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER APPLICATION NUMBER: 60/057,659
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 342, Application US/09328111 Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(669)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-342
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Best Local Similarity 100.0
Matches 18; Conservative
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Best Local Similarity 100.0
Matches 18; Conservative
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ORGANISM: Homo sapiens
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US-09-328-111-342/c
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Conservative
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: TMLR CLONE: 292810
                                                                                                 USA
                                                                                                                   94304
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LENGTH: 979
                                                                                                 COUNTRY:
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APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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APPLICANT: Gueglar, Karl P.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN A MIXED
TITLE OF INVENTION: LYMPHOCYTE REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 18; DB 4; Length 759; 100.0%; Pred. No. 83; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LAND E. MALTY, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHORE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFFWARE: WORD FELLO-
SOFFWARE: WORD DATA:
CURRENT APPLICATION DABER: US/09/276,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08567816A Patent No. 5780268 GENERAL INFORMATION:
                                     Sequence 71, Application US/09276531
Sequence 71, Application US/09276531
Patent No. 6183968
GENERAL INFORMATION:
                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
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LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 18; Conservative
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; CLONE: 1506088
US-09-276-531-71
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                       US-09-276-531-71/c
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RESULT 16
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NUMBER OF SEQUENCES:
ADDRESSES INVETE PRIMAMCEUTICALS, INC.
STREET: 3174 DOI:10 TO 10 TO 1
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Gaps

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Query Match 1.0%; Score 18; DB 4; Length 1568; Best Local Similarity 100.0%; Pred. No. 81; Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 81;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              0; Indels
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APPLICANT: Tung, Fong M.

APPLICANT: Cathrine, Strader D.

TITLE OF INVENTION: Human Neurokinin-1 Receptor

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
           NAME/KEY: sig_peptide
LOCATION: 75..1004
LOTER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.4
OTHER INFORMATION: seg VLILLFSLALIIL/PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/08117965
Patent No. 5484886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NICHOLSON, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25,147
ER: 18387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Merck & Co., Inc.
P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Nicholson, William H. REGISTRATION NUMBER: 25,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
                                                                                                                                                                                                                                                                                                                                                                                                        1859 AGCTGAAAAAAAAAA 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1177 GCCGCCTGGAGACCACCA 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1679 base pairs
nucleic acid
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Best Local Similarity 100.(
Matches 18; Conservative
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                                                                                                                    FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1536..1541
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rahway
: New Jersey
                                                                                                                                                                                                         ; NAME/KEY: polyA_site
; LOCATION: 1553..1568
US-09-247-155-68
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ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE:
US-08-117-965-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                  Gaps
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Patent No. 6380362

GENERAL INFORMATION:
APPLICANT: Watson, James D

APPLICANT: Watson, James G.
TITLE OF INVENTION: Polynuclectides, polypeptides expressed

TITLE OF INVENTION: Py the polynuclectides and methods for their use.
FILE REFERENCE: 11000,1050u1

CURRENT APPLICATION NUMBER: US/09/724,864

CURRENT APPLICATION NUMBER: US. No. 6380362 60/171,678

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0
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1.0%; Score 18; DB 4; Length 1261;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                            Query Match
1.0%; Score 18; DB 4; Length 979;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REPERENCE: GENERT.021A
CURRENT FILING DATE: 1999-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-05
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-10-04
NUMBER: OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-247-155-68
; Sequence 68, Application US/09247155A
; Patent No. 6312922
                                                                                                                                                 1857 TCAGCTGAAAAAAAAA 1874
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 75..1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER SOFTWARE: FASTS SEQ ID NO 34
  , ОКСАМТСТ...
US-09-288-143-52
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LENGTH: 1568
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US-09-364-230-19

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Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Anny TONGTONG
APPLICANT: AND METHODS FOR THERAPY OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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100.0%; Pred. No. 80;
Live 0; Mismatches 0; Indels
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McNoill, Patricia D.
MCNOILLON COMPOSITIONS AND METHODS FOR THE THERAPY
VVENTION: COMPOSITIONS OF LUNG CANCER
NVENTION: AND DIAGNOSIS OF LUNG CANCER
NVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.0%; Score 18; DB 4; Length 1844;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels
1.0%; Score 18; DB 4; Length 1797;
100.0%; Pred. No. 80;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/123,912A CURRENT APPLICATION NUMBER: US/09/123,912A CURRENT FILING DATE: 1998-07-27 PRIOR APPLICATION NUMBER: 09/040,802 PRIOR FILING DATE: 1998-03-18 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                           Sequence 88, Application US/09123912A Patent No. 6312695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 88, Application US/09643597
; Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Kanger, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: AND DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1859 AGCTGAAAAAAAAAA 1876
                                                                                         1859 AGCTGAAAAAAAAAA 1876
                                                                                                                   1770 AGCTGAAAAAAAAAAAA 1787
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Fan, Liqun
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
      Query Match
Best Local Similarity
Matches 18; Conserva
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; APPLICANT: Wang, TC
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US-09-123-912-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cahoon, Rebecca E.
APPLICANT: Chiney, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: RafalsKi, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
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100.0%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
ADDRESSEE: SCOtt J. Meyer, Monsanto Co., A3SD
STREET: 800 N. Lindbergh Blvd.
                                                                                                APPLICANT: Krause, James E.
TITLE OF INVENTION: Human Substance P Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. w..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-24(776)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US92/06532 FILING DATE: 19920805
                                              Sequence 2, Application PC/TUS9206532
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09364230 Patent No. 6348339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24
TELECHONDICATION INFORMATION:
TELEPHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1265 GCCGCCTGGAGACCACCA 1282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 1766 base pairs
NUCLEIC ACID
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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211..1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Oryza sativa
                                                                                                                                                                                                        STREET: 800 N. Li
CITY: St. Louis
STATE: Missouri
COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                             63167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
PCT-US92-06532-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 19
LENGTH: 1797
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                                    PCT-US92-06532-2
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TYPE: DNA ORGANISM: HUMAN
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US-08-837-199A-11
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LENGTH: 1929
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COCATION: (538)..(1926)
COTHER INFORMATION:
NAME/KEY: misc_feature
COCATION: (1)..(537)
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
NAME/KEY: misc_feature
NAME/KEY: misc_feature
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
COTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
                                                                                                                                                                             Sequence 9, Application US/08837199A

Fatent No. 6455277

GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: WEN, DIANZHI

TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C

CURRENT APPLICATION NUMBER: US/08/837,199A

CURRENT APPLICATION NUMBER: US 60/015,907

FRIOR FILING DATE: 1996-04-22

PRIOR FILING DATE: 1996-04-22

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: FIG, SHOOJAN.
APPLICANT: FIG, SHOOJAN.
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR FILE REFERENCE: A 4 01C
CURRENT APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1995-04-14
PRIOR FILING DATE: 1996-05-09
PRIOR FILING DATE: 1996-05-09
PRIOR FILING DATE: 1996-05-09
PRIOR FILING DATE: 1996-05-09
NUMBER: OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LENGTH: 1927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/08837199A
Patent No. 6455277
1859 AGCTGAAAAAAAAAA 1876
                           405 AGCCTGGCATCCGGCCTG 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-837-199A-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1927
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; NAME/KEY: misc_feature
; LOCATION: (1)..(539)
: OTHER INFORMATION: No. 6455277e= "1 to 539 is -237 to 301 of Figure 5 21bcon"
US-08-837-199A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: FOX, GARY M.
APPLICANT: JUNG, SHUGIAN
APPLICANT: WEN, DUANGII
ITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/08/837,199A
CURRENT FILING DATE: 1997-04-14
PRIOR PILING DATE: 1996-04-22
PRIOR PELICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
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; LOCATION: (550)..(550); OTHER INFORMATION: N in position 550 indicates any nucleic acid US-08-837-199A-40
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80;
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100.0%; Pred. No. 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08837199A Patent No. 6455277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/08837199A ; Sequence 41, Application US/08837199A ; Patent No. 645527 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                         718 AGCCTGGCATCCGGCCTG 735
                                                                                                                                                                                                                                                                                                                                                                                  405 AGCCTGGCATCCGGCCTG 422
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OTHER INFORMATION:
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LOCATION: (1)..(539)
OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"
NAME/KEY: misc_feature
LOCATION: (2078)..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between OTHER INFORMATION: ferent receptor clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
| CCATION: (2256)..(2294)
| COTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence
| OTHER INFORMATION: Ween different receptor clones
| NAME/KEY: misc_feature
| LOCATION: (1091)..(1091)
| COTHER INFORMATION: N in position 1091 indicates any nucleic acid
| US-08-837-199A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: FOX, GARY M.
APPLICANT: WEN, DUANGHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REPERBNCE: 4401C
CURRENT APPLICATION NUMBER: US/08/837,199A
CURRENT FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR PELING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
                                           APPLICANT: JING, SHUQIAN
APPLICANT: WEN, DUANZHI
TILLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A - 401C
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OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hsgr-2lbf"
NAME/KEY: misc_feature
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                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/837,199A
CURRENT FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR APPLICATION NUMBER: US 60/017,221
SOFTWARE: PATENTIN VOS: 47
SOFTWARE: PATENTIN VOS: 47
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; Sequence 37, Application US/08837199A
; Patent No. 6455277
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NUMBER OF SEQ ID NOS: 47
SOFWARE: Patentin version 3.1
SEQ ID NO 3.09
LENGTH: 3209
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OTHER INFORMATION:
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
LENGTH: 3209
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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LOCATION: (2107).
OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
OTHER INFORMATION: (2241).
OTHER INFORMATION: (2241).
OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones
NAME/KEY: misc_feature
LOCATION: (2250)...(2250)
OTHER INFORMATION: N in position 2250 indicates a position of divergence between di
OTHER INFORMATION: ferent receptor clones
NAME/KEY: misc_feature
OTHER INFORMATION: ferent receptor clones
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OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence be OTHER INFORMATION: tween different receptor clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: 507, GARY M.
APPLICANT: FOX, GARY M.
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A 4 01C
CURRENT APPLICATION NUMBER: US/08/837,199A
CURRENT PILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR FILING DATE: 1996-09-22
PRIOR FILING DATE: 1996-09-32
PRIOR FILING DATE: 1996-09-33
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2568
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                                                                           1.0%; Score 18; DB 4; Length 1929;
100.0%; Pred. No. 80;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08837199A Patent No. 6455277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 AGCCTGGCATCCGGCCTG 422
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                                                                                                                                       18; Conservative
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                                                                                   Query Match
Best Local Similarity
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ORGANISM: HUMAN
        ; ORGANISM: HUMAN
US-08-837-199A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
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US-08-837-199A-5
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US-08-837-199A-1
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NAME/KEY: unsure

LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,

COTHER INFORMATION: a, t, c, g, or other

US-09-484-970B-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 18; DB 4; Length 4478; 100.0%; Pred. No. 78; ve 0; Mismatches 0; Indels
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100.0%; Pred. No. 77;
ive 0; Mismatches 0; Indels
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; Patent No. 6376751
; GENERAL INFORMATION:
; APPLICANT: Sung, Z. Renee
; APPLICANT: Chen, Lingjing
; APPLICANT: The Regents of the University of California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484, 970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEO ID NOS: 172
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 106, Application US/09484970B
; Patent No. 6426186
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                                                                                                                                                        NAME/KEY: exon
LOCATION: (3495)..(4478)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (262)..(1659)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (2646)..(3329)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.09
Best Local Similarity 100.0
Matches 18; Conservative
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Best Local Similarity 100.C
Matches 18; Conservative
                                                                                                                 LOCATION: (3330)..(3381)
OTHER INFORMATION:
                                                  . (2645)
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Intron
LOCATION: (3382)..(3494)
CTHER INFORMATION:
US-09-513-057C-26
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                                             LOCATION: (1660)..
OTHER INFORMATION:
NAME/KEY: exon
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APPLICANT: Jones, 1
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US-09-415-946-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1091)..(1091)
OTHER INSC_MANTION: N in position 1091 indicates any nucleic acid.
CATHORNATION: Q1079..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between diff OTHER INFORMATION: N in position 2078 indicates a position of divergence between diff OTHER INFORMATION: (2256)..(2294)
COTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence between different receptor clones.
COTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence between different receptor clones.
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Patent No. 643321
Patent No. 643321
Patent No. 643321
APPLICANT: Wagner, et al.
TITLE OF INVENTION: GENER REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
FILE REFERENCE: 1505-54357
CURRENT APPLICATION NUMBER: US/09/513,057C
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
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US-09-651-011A-3
US-09-651-011A-3
Sequence 3, Application US/09651011A
Sequence 3, Application US/09651011A
Patent No. 6346416
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. COWSETT
TITLE OF INVENTION: ANTIENSE MODULATION OF HPK/GCK-LIKE KINASE EXPRESSION
FILE REFERENCE: RTS-0168
CURRENT APPLICATION NUMBER: US/09/651,011A
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.0%; Score 18; DB 4; Length 4266; Best Local Similarity 100.0%; Pred. No. 78; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  720 AGCCTGGCATCCGGCCTG 737
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; LOCATION: (1)...(3528)
US-09-651-011A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(261)
OTHER INFORMATION:
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LENGTH: 4478
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GENERAL INCORNATION:
APPLICANT: Sung, Z. Renee
APPLICANT: Sung, Z. Renee
APPLICANT: Aubert, Dominique
APPLICANT: Chen, Lingjing
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/415,946
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0
                       11.0%; Score 18; DB 2; Length 10079; 100.0%; Pred. No. 75; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/476,866
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DAIL.
CLASSIETCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/322,766
FILING DATE: 13-0CT-1994
APPLICATION NUMBER: US 08/136,207
                                                                                                                                                                                         E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 20:
SERVITUATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09415946; Patent No. 6376751
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Best Local Similarity 100.0%; P:
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,9
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; LOCATION: 5086..5803
US-08-476-866-20
                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
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STRANDEDNESS: sing
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         GENERAL INFORMATION:
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US-09-415-946-1
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TITLE OF INVENTION: Nucleic Acids That Control Reproductive Development in TITLE OF INVENTION: Plants
FILE REFERENCE: 018941-000110US
CURRENT APPLICATION NUMBER: US/09/415,946
CURRENT FILING DATE: 1999-10-08
PRIOR PAPLICATION NUMBER: US 09/169,696
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.0%; Score 18; DB 4; Length 8648;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             OTHER INFORMATION: EMF1 gene and its promoter region
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US-08-476-866-20
; Sequence 20, Application US/08476866
; Patent No. 5994339
                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                                                                             PatentIn Ver. 2.1
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OTHER INFORMATION: exon 7
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OTHER INFORMATION: exon 4
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OTHER INFORMATION: exon 5
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OTHER INFORMATION: exon 1
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                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter
LOCATION: (1)..(3201)
NAME/KEY: CDS
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LENGTH: 8648
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NAME/KEY:
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OTHER INFO
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1.0%; Score 18; DB 4; Length 84495;
100.0%; Pred. No. 68;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/342,411A FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-342-411A-32
Sequence 32, Application US/08342411A
Sequence 32, Application US/08342411A
Sequence 32, Application US/08342411A
Seturn No. 5639616
GENTRAL INFORMATION:
APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
TITLE OF INVENTION: USPORTIONS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
FILE REFERENCE: CLOO1151CIP
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEO for ...
                                                                                                                         FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
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NAME: KITCHELL, BARBARA S.
RECISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   1859 AGCTGAAAAAAAAAAA 1876
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(713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1024 CCTGTGACCTGAGGATC 1040
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 18; Conserva
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                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                          SEQ ID NO 3
LENGTH: 84495
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US-08-342-411A-32
                                                                                                                                                                                                                                                                                             ; OTHER INFORM
US-09-797-906-3
                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
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Fatent No. 6329188
GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
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                                                                                                                                                                                                           OTHER INFORMATION: genomic DNA (Ecotype Columbia) from CD82 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                               LOCATION: join(4241..4335, 4448..4623, 4704..4823, 4903..4956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 18; DB 4; Length 17341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. />;
Matches 18; Conservative 0; Mismatches
  CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,696
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                          TYPE-
TYPE- DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1840 GGGTATTAAATTATGAAT 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1130 GGGTATTAAATTATGAAT 1147
                                                                                        PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                       LOCATION: (3202)..(3265)
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (4160)..(4335)
OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (4903)..(4956)
OTHER INFORMATION: exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: exon 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: exon 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (6448)..(8065)
OTHER INFORMATION: exon 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: exon 8
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LOCATION: (4336)..(4447)
                                                                                                                                                                                                                                                                                                                                                                                                                        (3266)..(4159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: intron
LOCATION: (4824)..(4902)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: intron Incartion: (4957)..(5045)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4448)..(4623)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: intron
LOCATION: (6308)..(6447)
NAME/KEY: exon
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LOCATION: (8066)..(8300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (4704)..(4823)
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                                                                                                                                                                                                                                NAME/KEY: promoter LOCATION: (1)..(3201)
NAME/KEY: CDS
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LOCATION: (3266).
NAME/KEY: exon
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                                                                                                                               17341
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US-09-797-906-3
                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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0.9%; Score 17; DB 5; Length 42; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: H. Robert Horvitz et al.
TILLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/216001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-7045
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                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: MacIntosh 6.0.5
SOFTWARE: Microsoft Word 4.00B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/588,21
FILING DATE: January 12, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %3-08-588-258B-21
; Sequence 21, Application US/08588258B
; Patent No. 5929207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Clark & Elbing LLP STREET: 176 Federal Street
                                                                                                                                                                                                                     PRIOR APPLICATION DATA: None
ATTORNEY/AGENT INPORMATION:
NAME: Lunn, Paul, G
REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: JB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7255
TELEFAX: 201-822-7039
TELEEX: 211465
INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 198 base pairs
TYPE: nucleic acid
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Best Local Similarity 100.0
...-hes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 42 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                          19930326
                     COMPUTER READABLE FORM:
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                                                                                                                                                                               FILING DATE:
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07940
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PCT-US93-02612-7
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APPLICANT: Hesson, Thomas
APPLICANT: Mannarino, Anthony
TITLE OF INVENTION: Monomeric Platelet-Derived Growth Factor and Prevention of
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                       UBIQUITOUS NUCLEAR RECEPTOR: COMPOSITIONS AND METHODS
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 17; DB 5; Length 29; 100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: PC-TOS/MS-DOS/ASCII
APPLICATION NUMBER: PCT/US94/12883
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
FILING DATE: 10-NOV-1993
FILING DATE: 10-NOV-1993
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One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHELL
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154P--
TELECOMMUNICATION INFORMATION:
TELECHONE: (512) 418-3000
TELEFRY: (713) 789-2679
                                                                                                                                                                                   TITLE OF INVENTION: UBIQUITOUS NUCLITITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSE: ADDRESSEE: ALOId, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-1893-02612-7/c; Sequence 7, Application PC/TUS9302612; GENERAL INFORMATION:
                                                                                                                Sequence 32 Application PC/TUS9412883 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-12883-32
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TELEFAX: (715,
TELEFAX: 0.000 132
TELEFAX: 0.000 132
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TENGTH: 20 base pairs
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Best Local Similarity 100.0
Matches 17; Conservative
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              13 CCTGTGACCTGAGGATC 29
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STATE: New Jers
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                   Houston
                                                                                                                                                                                                                                                                                                                                                           STATE: Texas
COUNTRY: Unit
ZIP: 77210
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                                                                                                       PCT-US94-12883-32
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0
                                                                                                 Length 198;
                                                                                 Query Match 0.9%; Score 17; DB 2; Length 198 Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 17; DB 3; Length 198; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/08460505
Patent No. 6069296
GENERAL INFORMATION:
APPLICANT: Horvitz, Robert H.
APPLICANT: Koelle, Michael
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SECURNES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/460,505
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01997/214001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish Richardson P.C. STREET: 225 Franklin Street CITY: Boston
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PCT-US96-08295-21
Sequence 21, Application PC/TUS9608295
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-588-258B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-460-505-21
                                                                                                                                                                      1451 TGCCCAGGAGCACATCT 1467
                                                                                                                                                                                             174 TGCCCAGGAGCACATCT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1451 TGCCCAGGAGCACATCT 1467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.9%
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                              US-08-460-505-21
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                                                                                                                                                                                                                                                                                 RESULT 44
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APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08295
FILING DATE: 31-MAY-1996
CLASSIFICATION DATA:
APPLICATION ON STA:
APPLICATION NUMBER: US 08/588,258
FILING DATE: 12-JAN-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        39,109
39,109
RER: 01997/216001
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                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/08518878B Patent No. 5702902 GENERAL INFORMATION: APPLICANT: Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) PCT-US96-08295-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1451 TGCCCAGGAGCACATCT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 TGCCCAGGAGCACATCT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: COTUZZI, LAUTA A. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5'
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: 23-AUG
                                                                     02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 10036-2711
                    Boston
                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-518-878B-34
                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                       STATE:
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STATE:
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GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
TITLE OF INVENTION:
                                             Sequence 34, Application US/08807861A
Sequence 34, Application US/08807861A
Sequence 34, Application US/08807861A
GENERAL INFORMATION:
APPLICANT: TATAGATICANT:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 17; DB 2; Length 457;
100.0%; Pred. No. 2.4e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk compatible operating system; PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A FILING DATE: 26-FEB-1997 CLASSIFICATION: 51"
PRIOR APPLICATION: 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1155 Avenue of the Americas
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLEASTEICATION: ...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
APLICATION NUMBER: US 08/518,878
FTLING DATE: 23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
APPLICATION DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COFUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/08470868A Patent No. 5861485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1860 GCTGAAAAAAAAAA 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 GCTGAAAAAAAAAAAAA 457
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nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown US-08-807-861A-34
                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-470-868A-34
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                          RESULT 48
US-08-807-861A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
WUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                   0.9%; Score 17; DB 1; Length 457; 100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,522B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7853-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA N. 7853-0
REFERENCE/DOCKET NUMBER: 7853-0
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEC ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/08294522B
Patent No. 5741666
             TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1860 GCTGAAAAAAAAAAA 1876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 457 base pairs
                                                                                                                                                                                                                                                                                                                                                  Ouery Match 0.9%
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                , TOPOLOGY: unknown
US-08-518-878B-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
US-08-294-522B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Gaps

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APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
                                                                                                                                                                                                                                                     ATCHARTAGENT INFORMATION:

NAME: COUZZI, LALIZA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 30,742

TELECOMMUNICATION INPORMATION:

TELEPHONE: (212) 790-9990

TELERA: (212) 869-864

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 base pairs

SEQUENCE CHARACTERISTICS:

LENGTH: 457 base pairs

TYPE: nucled: acid

TYPE: nucled: acid

TYPE: nucled: acid

TOPOLOGY: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-UN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1860 GCTGAAAAAAAAAA 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-210-681-34
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 29, 2002, 01:15:08
REFERENCE/DOCKET NUMBER: 7853-066
              TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                           1860 GCTGAAAAAAAAAAA 1876
                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.(
Matches 17; Conservative
                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                               Job time : 282 secs
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                      US-09-210-681-34
                                                                                                                                                                                                                            Query Match
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Sequence 103, App Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 51, Appl Sequence 104, App Sequence 104
                                                                                                                                                                        Sequence 53, Appl
Sequence 103, App
Sequence 103, Appl
S
  Sequence 321, App
Sequence 53, Appl
                                                                                                                                                           Sequence
US-09-944-41-321

US-09-944-413-53

US-09-944-403-53

US-09-944-944-53

US-09-944-944-53

US-09-944-944-53

US-09-944-457-53

US-09-944-475-53

US-09-944-475-53

US-09-944-475-53

US-09-944-475-53

US-09-944-475-53

US-09-944-13-103

US-09-944-13-103

US-09-944-13-103

US-09-944-473-53

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US-09-944-473-103

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US-09-944-444-473-104

US-09-944-444-473-104

US-09-944-444-473-104

US-09-944-443-104
          Sequence 49, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
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Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
                                                                                                                                     ; Search time 129 Seconds
(without alignments)
5907.719 Million cell updates/sec
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                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_pUBCOMB.seq:*
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3: /cgn2_6/ptodata/2/pubpna/PCT_MEM_PUB.seq:*
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PRIOR RELIKED NATE: DECEMBER 16,1997
PRIOR FILIKE DATE: DECEMBER 16,1999
PRIOR PRIOR FILIKE DATE: DECEMBER 17,2000
PRIOR PRIOR DATE: DATE: DATE: DATE
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PRIOR FILIKE DATE: PEDIUAR 2, 2000
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RESULT 2
US-09-944-403-49
; Sequence 49, Application US/09944403
; Patent No. US20020165143A1
; GENERAL INFORMATION:
APPLICANT: Backer, Kevin
APPLICANT: Bottein,David
; APPLICANT: Eaton,Dan
APPLICANT: Gerrara,Napoleone
APPLICANT: Gerrara,Napoleone
; APPLICANT: Gerrara,Napoleone
; APPLICANT: Goddard,Audrey
; APPLICANT: Goddard,Audrey
; APPLICANT: Goddowski,Paul

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TYPE: DNA
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                                                                                                                                                                            BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
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FILING DATE: No. US20020165143A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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                                                                                                                                                                     TITLE OF INVENTION: ACCES AND TRANSMEMBRA, TITLE OF INVENTION: ACCES ENCODING THE SAME FILE REFERENCE: P5548PL1
CURRENT FILING DATE: 2001-05-26
CURRENT FILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: PEDIULATY 9, 1998
PRIOR FILING DATE: DECEMBER 16/1058
PRIOR PELICATION NUMBER: POT/US98/1510
PRIOR FILING DATE: DECEMBER 16/1058
PRIOR PELICATION NUMBER: POT/US98/1510
PRIOR FILING DATE: DECEMBER 16/1058
PRIOR PELICATION NUMBER: POT/US98/1255
PRIOR PELICATION NUMBER: POT/US98/1255
PRIOR FILING DATE: DECEMBER 16/1059
PRIOR FILING DATE: SEPTEMER 16/1059
PRIOR FILING DATE: SE
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
                                                                   Kljavin, Ivar
                                                                                                             Roy, Margaret
Tumas, Daniel
                                                                                                                                                            Wood, William
                                                                                           Napier, Mary
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APPLICANT:
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                                PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: MATCH 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 28, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER 1, 2000
PRIOR FILING DATE: DECEMBER 1, 2000
PRIOR FILING DATE: PECEMBER 1, 2000
PRIOR FILING DATE: PECEMBER 1, 2001
                  FILING DATE: February 11, 2000 APPLICATION NUMBER: PCT/US00/04414
APPLICATION NUMBER: PCI/US00/03565
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Best Local Similarity
Matches 1876; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRICR APPLICATION NUMBER: 09/866,028
PRICR FILING DATE: 2001-05-25
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PRIOR FILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: PEDTUATY 5, 1998
PRIOR FILING DATE: FEDTUATY 5, 1998
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PRIOR FILING DATE: FEDTUATY 26, 1998
PRIOR FILING DATE: FEDTUATY 27, 1998
PRIOR FILING DATE: PECTUATY 27, 1998
PRIOR FILING DATE: PEDTUATY 28, 1999
                                                                                                                                                                                                                                                                                                                                                         Sequence 49, Application US/09944896 Patent No. US20020168715A1 GENERAL INFORMATION:
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Napier, Mary
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US-09-944-896-49
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APPLICATION NUMBER: PCT/US98/19330

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tive 0; Mismatches
OR FILING DATE: September 16, 1998
OR APPLICATION NUMBER: PCT/US98/25108
OR PILING DATE: December 1, 1998
OR PPLICATION NUMBER: 09/216,021
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MAICH 3, 1999
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PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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ORGANISM: Homo Sapien
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             AACTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCC 420
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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
                                                              1501 CATGGCTCCCTCGCCTGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACTGTCT 1560
  1441 TCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCA 1500
                                         1501 CATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCCTTACCTGTCTGCCCACCTGTCT 1560
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CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069334

PRIOR FILING DATE: December 11, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

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PRIOR APPLICATION NUMBER: 60/069,696
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APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
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Grimaldi,Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
Kljavin, Ivar
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APPLICANT: Botstein, David
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APPLICATION NUMBER: PCT/US99/28301
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PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR APPLICATION NUMBER: 09/216, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: DECEMBER: 09/254,311
PRIOR FILING DATE: JUNE 22, 1999
PRIOR FILING DATE: JUNE 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. USZ0020173463Alember
PRIOR FILING DATE: No. USZ0020173463Alember
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PEDUALY 11, 2000
PRIOR FILING DATE: FEBUARY 22, 2000
PRIOR FILING DATE: MATCH 2, 2000
PRIOR FILING DATE: MATCH 30, 2000
PRIOR PRIING DATE: MATCH 30, 2000
PRIOR PRIING DATE: MATCH 30, 2000
PRIOR PRIING DATE: PEDUALY 18, 2000
PRIOR PRIING DATE: PEDUALY 12, 2000
PRIOR PRIING DATE: PEDUALY 28, 2000
PRIOR PRIOR FILING DATE: PEDUALY 28, 2001
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/075,945
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 16, 1997 APPLICATION NUMBER: 60/069,870
                                                                                                                                                                                                                                APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/112,850
                                                         FILING DATE: December 17, 1997 APPLICATION NUMBER: 60/069,873
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Best Local Similarity 100.0
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US-09-944-944-49
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Patent No. US20020058309A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Hillan, Kenneth
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Eaton, Dan
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     APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT PAPLICATION NUMBER: US/09/866,028
CURRENT FILNG DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
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APPLICANT: Tumas, Daniel
                                                                                                                                                   ORGANISM: Homo Sapien
                                                                                                                           LENGTH: 1876
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                                                                                                                                          TYPE: DNA
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781 ATGCAGGGGGCCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG 840
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                           GACGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US98/25108
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: EPECTUARY 9, 1998
PRIOR FILING DATE: SEDTUARY 9, 1998
PRIOR FILING DATE: FEDTUARY 9, 1998
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DR APPLICATION NUMBER: 60/074,092
DR FILING DATE: February 9, 1998
DR APPLICATION NUMBER: 60/075,945
DR FILING DATE: February 25, 1998
DR APPLICATION NUMBER: 60/112,850
DR APPLICATION NUMBER: 60/112,296
DR APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: 09/216, 021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
                     Sequence 49, Application US/09944449
Patent No. US20020102647A1
GENERAL INFORMATION:
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Gurney, Austin
Hillan, Kenneth
                                                                                                                                                                                                          Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                  Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
                                                                                                            APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kljavin, Ivar
Napier, Mary
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Wood, William
                                                                                                                                                                              Eaton, Dan
US-09-944-449-49
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                                                                                                    FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020102647Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020102647Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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100.0%; Pred. No. 0;
ive 0; Mismatches
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PRIOR APPLICATION NUMBER: PC1/0500/0414
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: PCD. 12, 2000
PRIOR PELICATION NUMBER: PCT/USO0/0541
PRIOR PELICATION NUMBER: PCT/USO0/08419
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 28, 2000
PRIOR PILING DATE: UNWBER: PCT/USO0/20710
PRIOR PILING DATE: UNWBER: PCT/USO0/32678
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: Ebcember 1, 2000
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                        FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
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Best Local Similarity 100.
Matches 1876; Conservative
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ORGANISM: Homo Sapien
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1681 AGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740
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1561 GGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 1620
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APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
                                                                                1681 AGAAGAAGCTGGGCCCCTTCGCCTTTTGATTGGGAAGATGGCTTCAATTAGATGGC
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CURRENT PELING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/966,028
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR PELING DATE: December 3, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR PLING DATE: December 11, 1997
PRIOR PLING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
Kilavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
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APPLICANT: Botstein, David
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         PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: December 19, 1997
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR PILING DATE: JOURNALY 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR PILING DATE: February 9, 1998
PRIOR PLING DATE: February 25, 1998
PRIOR PLING DATE: February 25, 1998
PRIOR PLING DATE: February 25, 1998
PRIOR PLING DATE: PECEMBER: 60/113, 296
PRIOR PLING DATE: PECEMBER: 60/113, 296
PRIOR PLING DATE: December 16, 1998
PRIOR PLING DATE: December 17, 1998
PRIOR PLING DATE: December 16, 1998
PRIOR PLING DATE: December 17, 1999
PRIOR PLING DATE: December 17, 1999
PRIOR PLING DATE: December 15, 1999
PRIOR PLING DATE: PEPURATION NUMBER: PCT/US99/2009
PRIOR PLING DATE: DECEMBER: PCT/US99/30095
PRIOR PLING DATE: DECEMBER: PCT/US99/30095
PRIOR PLING DATE: DECEMBER: PCT/US99/30095
PRIOR PLING DATE: PEPURATY 11, 2000
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PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
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US-09-944-457-49
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1201 CTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGG 1260
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
                                                                                                                             1381 TGCAGGCTTCAGCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACA
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Patent No. US20020127643A1
GENERAL INFORMATION:
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Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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Hillan, Kenneth
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CURRENT APPLICATION NUMBER: US/09/945,587

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FILING DATE: No. US20020127643Alember 30, APPLICATION NUMBER: PCT/US99/28313 FILING DATE: No. US20020127643Alember 30, APPLICATION NUMBER: PCT/US99/28301
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R APPLICATION NUMBER: PCT/US00/08439
R FILING DATE: March 30, 2000
R RAPLICATION NUMBER: PCT/US00/14042
R FILING DATE: MAY 22, 2000
R APPLICATION NUMBER: PCT/US00/20710
R RILING DATE: July 28, 2000
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: PCT/US00/04414
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R APPLICATION NUMBER: 09/216 021
R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 09/218 517
R FILING DATE: December 22, 1998
R APPLICATION NUMBER: 09/254,311
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APPLICATION UNDBER: 60/074,086
FILING DATE: FEBTUARY 9, 1998
APPLICATION NUMBER: 60/074,092
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FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
                                                                            APPLICATION NUMBER: 60/067,411
FILING DATE: December 3, 1997
APPLICATION NUMBER: 60/069,334
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APPLICATION WUMBER: 60/066,278
FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,425
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FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/069,702
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FILING DATE: December 18, 1997
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APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: 60/146,222
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                          APPLICATION NUMBER: 09/866,028
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APPLICATION NUMBER: 60/069,694
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PRIOR APPLICATION NUMBER: PCT/USOO/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
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Best Local Similarity 100.0%;
Matches 1876; Conservative 0;
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                                                                           GACGTCTCAACATCAGCACTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACT
                                  GCCAAGTGAGGTGCAGCCTGCAGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/945,015
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: PEDIUATY 9, 1998
PRIOR FILING DATE: PEDIUATY 25, 1998
PRIOR FILING DATE: December 16, 1998
Sequence 49, Application US/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Grimaldi, Christopher
                                                                                                                                                                  Ferrara, Napoleone
Filvaroff, Ellen
                                                                                   APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Hillan, Kenneth
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Goddard, Audrey
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Napier, Mary
Roy, Margaret
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PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR PILING DATE: No. US20020132768Alember 30, 1999
PRIOR FILING DATE: No. US20020132768Alember 30, 1999
PRIOR FILING DATE: No. US20020132768Alember 30, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR PRILOR APPLICATION NUMBER: PCT/US99/28301
PRIOR PLICATION NUMBER: PCT/US99/3005
PRIOR FILING DATE: Pechcuary 11, 2000
PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
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PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR FILING DATE: JULY 28, 2000
PRIOR PELING DATE: JULY 28, 2000
PRIOR PAPLICATION NUMBER: PCT/USO0/20710
PRIOR PELING DATE: December 1, 2000
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Best Local Similarity 100.8
Matches 1876; Conservative
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CORGANISM: Homo Sapien
US-09-945-015-49
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APPLICATION NUMBER: PCT/US99/12252

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APPLICANT: GOGGWASI, Paul
APPLICANT: GOLOWSI, Paul
APPLICANT: GUINCY, AUSTIN
APPLICANT: Hillan, Kenneth
APPLICANT: Najavin, Ivar
APPLICANT: Najavin, Ivar
APPLICANT: Najavin, Ivar
APPLICANT: Najavin, Ivar
APPLICANT: Nojec, Margaret
APPLIC
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1681 AGAAGAAGCTGGGGCCCTTCGCCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740
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Patent No. US20020132981A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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US-09-944-396-49
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                    181 TCCTTGGCACCACCAGGCAGGAGGTGTGCCACCCCAGCTGCAGGAGCAGGCTCCGATGG
                                                                              241 CCGGAGCCCTGAACAGGAAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCA
                                                                                                 141 CCGGAGCCCTGAACAGGAAGGAGGTTTCTTGCTCCTCTCCCTGCACAACGCCTGCGCA
                                                                                                                                                           301 GCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCC
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                                                       PRIOR PELLICATION NUMBER: 00/075,945
PRIOR APPLICATION NUMBER: 00/075,945
PRIOR APPLICATION NUMBER: 00/075,945
PRIOR APPLICATION NUMBER: 00/112,850
PRIOR PELIGATION NUMBER: 00/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR PELICATION NUMBER: 00/114,229
PRIOR PELICATION NUMBER: 00/114,229
PRIOR APPLICATION NUMBER: 00/114,229
PRIOR APPLICATION NUMBER: 00/146,222
PRIOR APPLICATION NUMBER: 00/216,021
PRIOR APPLICATION NUMBER: 00/216,021
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 00/216,021
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PRIOR APPLICATION NUMBER: 00/216,021
PRIOR APPLICATION NUMBER: 00/216,311
PRIOR APPLICATION NUMBER: 00/216,311
PRIOR APPLICATION NUMBER: 00/216,311
PRIOR APPLICATION NUMBER: 00/10599/2813
PRIOR PILING DATE: MATCH 3, 1999
PRIOR PILING DATE: NO. 052002013291Alember 30, 1999
PRIOR PELING DATE: NO. 052002013291Alember 30, 1999
PRIOR PELING DATE: NO. 052002013291Alember 30, 1999
PRIOR PELING DATE: December 16, 1999
PRIOR PELING DATE: DECEMBER: PCT/US99/3005
PRIOR PELING DATE: DECEMBER: PCT/US90/0414
PRIOR PILING DATE: DECEMBER: PCT/US90/0414
PRIOR PILING DATE: DECEMBER: PCT/US90/0414
PRIOR PILING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0439
PRIOR PELING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0419
PRIOR PELING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/1404
PRIOR PELING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/1404
PRIOR PELING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0550
PRIOR APPLICATION NUMBER: PCT/US00/0500
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                        FILING DATE: February 9, 1998 APPLICATION NUMBER: 60/074,092
          APPLICATION NUMBER: 60/074,086
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                                              CTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGGGTTTGGCAACTGCGTGGAGC
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CURRENT FILING DATE: 2001-08-31
PRION APPLICATION NUMBER: 09/866,028
PRION FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Frivarcif, Ellen
APPLICANT: Frivarcif, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Godard, Audrey
APPLICANT: Godard, Paul
APPLICANT: Gimaldi, Christopher
APPLICANT: Gumed, Austin
APPLICANT: Hillan, Kenneth
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Napier, Mary
Roy, Margaret
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PRIOR FILING DATE: September 10, 1990
PRIOR FILING DATE: December 1, 1998
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PRIOR PLICATION NUMBER: 09/216,021
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999/254,311
PRIOR FILING DATE: March 3, 1999/254,311
PRIOR FILING DATE: March 3, 1999/254,311
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020133675Alember 30, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/38301
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 18, 1998
PRIOR FILING DATE: December 18, 1998
PRIOR FILING DATE: FEBRUARY 9, 1998
PRIOR FILING DATE: FEBRUARY 25, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: DECEMBER 16, 1998
PRIOR FILING DATE: DECEMBER 16, 1998
PRIOR FILING DATE: DECEMBER 16, 1998
PRIOR FILING DATE: SEPTUARY 9, 1998
PRIOR FILING DATE: POTTUGS84/19330
PRIOR FILING DATE: POTTUGS84/19330
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PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 21, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/USOO/05841
PRIOR APPLICATION NUMBER: PCT/USOO/05841
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR PRELICATION NUMBER: PCT/USOO/20710
PRIOR PRELICATION NUMBER: PCT/USOO/32678
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
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                       ORGANISM: Homo Sapien
LENGTH: 1876
TYPE: DNA
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                                               ACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACCTT
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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  US20020142419Alember 30, 1999
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                                       PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PELING DATE: PEDRUARY 11, 2000
PRIOR FILING DATE: FEBRUARY 21, 2000
PRIOR FILING DATE: FEBRUARY 22, 2000
PRIOR FILING DATE: FEBRUARY 22, 2000
PRIOR PILING DATE: MARCH 2, 2000
PRIOR PILING DATE: MARCH 2, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR FILING DATE: MAY 30, 2000
PRIOR PELING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR PILING DATE: MAY 22, 2000
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PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
                           APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 49
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Matches 1876; Conservative
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ORGANISM: Homo Sapien
  FILING DATE:
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                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020142419Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT FILING DATE: 2001-06-06
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APPLICATION NUMBER: PCT/US98/1930
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 00/669,334
PRIOR FILING DATE: DECEMBER 1, 1997
PRIOR FILING DATE: DECEMBER 1, 1997
PRIOR FILING DATE: DECEMBER 1, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR PELING DATE: DECEMBER 12, 1997
PRIOR PELING DATE: DECEMBER 12, 1997
PRIOR PELING DATE: DECEMBER 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR PELING DATE: PEDIUARY 25, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR PELING DATE: PEDIUARY 25, 1998
PRIOR PELING DATE: PEDIUARY 25, 1998
PRIOR PELING DATE: PEDIUARY 26, 1998
PRIOR PELING DATE: PEDIUARY 26, 1998
PRIOR PELING DATE: DECEMBER 16, 1998
PRIOR PELING DATE: DECEMBER 16, 1998
PRIOR PELING DATE: SEPTEMER 16, 1998
PRIOR PELING DATE: SEPTEMER 16, 1998
PRIOR PELING DATE: SEPTEMBER 16, 1998
PRIOR PELING DATE: MATCH 3, 1999
PRIOR PELING DATE: MATCH 3, 1999
PRIOR PELING DATE: MATCH 3, 1999
PRIOR PELING DATE: DECEMBER 16, 1999
PRIOR PELING DATE: DECEMBER 16, 1999
PRIOR PELING DATE: PERIOR PELING DATE: SEPTEMBER 16, 1999
PRIOR PELING DATE: DECEMBER 16, 1999
PRIOR PELING DATE: MATCH 3, 1999
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Grimaldi, Christopher
Ferrara, Napoleone
                                                                        Goddard, Audrey
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Hillan, Kenneth
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Roy, Margaret
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0 - O	GACGICICAACAICAGCACCIGCCACIGCCACIGICCCCCIGGCIACACGGGCAGAIACI 900
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0 - 0	GCGTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACAAGGTGCATTTTCCCTTCC 1020
4-4	ACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCT 1080
~ ~	ATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGTGCTGGCCCAGATCAAGAGC 1140
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	aatgecagaagttgggcagagaggcaggaggccagtgaggccagggagtgt 1680
a,	AGAAGAACCTGGGCCCCTTCGCTTTTGATTGGGAAGATGGCCTTCAATTAGATGGC 1740

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## APPLICANT: WOOG, WILLIAM
### TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
### TITLE OF INVENTION: SECRETED
### CLIDS ENCODING THE SAME
FILE REPERENCE: P3548PL01
CURRENT APPLICATION NUMBER: US/09/943,762
PRIOR FILING DATE: 2010-109-26
PRIOR FILING DATE: D010-165-25
PRIOR FILING DATE: D0-60-10,334
PRIOR FILING DATE: D0-60-11, 1997
PRIOR FILING DATE: P0-11, 1997
PRIOR FILING DATE:
                                                          1741 GAAGGAGAGACACCGCCAGTGGTCCAAAAAGGCTGCTCTTCTTCCACCTGGCCCAGACCC 1800
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                                                                                              Sequence 49, Application US/09943762
Patent No. US20020142958A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Tumas, Daniel
Wood, William
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Napier, Mary
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                                                                                GCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCC
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                     FRIOR APPLICATION NUMBER: 60/113, 296
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 12, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 23, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 17, 1999
PRIOR FILING DATE: September 17, 1999
PRIOR FILING DATE: September 17, 1999
PRIOR FILING DATE: September 17, 1999
PRIOR FILING DATE: No. US20020142958Alember 30, 1999
PRIOR FILING DATE: PECTURS99/28301
PRIOR PRILING DATE: PECTURS99/28301
PRIOR PRILING DATE: PECTURS99/30095
PRIOR PRILING DATE: PECTURS99/30095
PRIOR PRILING DATE: PECTURSY 11, 2000
PRIOR PRILING DATE: FEBRUARY 11, 2000
PRIOR PRILING DATE: FEBRUARY 22, 2000
PRIOR PRILING DATE: FEBRUARY 22, 2000
PRIOR PRILING DATE: MARCH 2, 2000
PRIOR PRILING DATE: MARCH 2, 2000
PRIOR FILING DATE: MARCH 3, 2000
PRIOR FILING DATE: MARCH 3, 2000
PRIOR FILING DATE: MARCH 3, 2000
PRIOR FILING DATE: PERCENTY 11, 2000
PRIOR PRIOR FILING DATE: PERCENTY 11, 2000
PRIOR PRIOR PRILING DATE: PERCENTY 21, 2000
PRIOR PRIOR PRILING DATE: PERCENTY 30, 2000
PRIOR PRILING DATE: PERCENTY 30, 2000
PRIOR PRIOR PRILING DATE: PERCENTY 30, 2000
PRIOR PRILING DATE: PECTURS 2000
PRIOR PRILING DATE: PECTURS 30, 32, 2000
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100.0%; Pred. No. 0;
Live 0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
        FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
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Matches 1876; Conservative
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US-09-943-762-49
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APPLICANT: Gutney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Wary
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Wood, Milliam
APPLICANT: Wood, Milliam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILL OF TATLE OF INVENTION: ACIDS ENCODING THE SAME
TILL OF DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 00/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: DECEMBER: 11, 1997
PRIOR FILING DATE: DECEMBER: 11, 1997
PRIOR FILING DATE: DECEMBER: 11, 1997
PRIOR PPLICATION NUMBER: 60/069334
PRIOR FILING DATE: DECEMBER: 11, 1997
PRIOR PPLICATION NUMBER: 60/069334
PRIOR PPLICATION NUMBER: 60/069354
1381 IGCAGGCTTCAGCTGCCTTCAACTGGAACGACCGCTGCAAAACCCGAAACCGTTACA 1440
                      1561 GGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 1620
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Patent No. US20020142959A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baten, David
APPLICANT: Eaton, Dan
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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PRIOR PLINK DATE: December 11, 1997
PRIOR APPLICATION WOMBER: 60/663/425
PRIOR APPLICATION WOMBER: 60/663/425
PRIOR APPLICATION WOMBER: 60/663/956
PRIOR PLINKS DATE: December 11, 1997
PRIOR PLINKS DATE: December 16, 1997
PRIOR PLINKS DATE: December 17, 1997
PRIOR PLINKS DATE: December 18, 1998
PRIOR PAPLICATION NUMBER: 60/704, 400
PRIOR PLINKS DATE: Becamber 19, 1998
PRIOR PAPLICATION NUMBER: 60/704, 1998
PRIOR PAPLICATION NUMBER: 60/705, 940
PRIOR PLINKS DATE: PAPL PS, 1998
PRIOR PAPLICATION NUMBER: 60/705, 945
PRIOR PLINKS DATE: PAPL PS, 1998
PRIOR PAPLICATION NUMBER: 60/713, 286
PRIOR PLINKS DATE: PAPL PS, 1998
PRIOR PAPLICATION NUMBER: 60/713, 286
PRIOR PLINKS DATE: PAPL PS, 1999
PRIOR PAPLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PAPLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PAPLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR DATE: NUMBER: PCT/US99/1309
PRIOR PRIOR PAPLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PRIOR DATE: PCT/US99/1309
PRIOR PRIOR PAPLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PAPLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PRIOR DATE: PCT/US99/1309
PRIOR PRIOR PAPLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PRIOR POLICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PURICATION NUMBER: PCT/US99/1309
PRIOR PRIOR PURICATION NUMBER: PCT/US99/
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Query Match 100.0%; Score 1876; DB 10; Length 1876; Best Local Similarity 100.0%; Pred. No. 0; Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 CTCTTTTGTCCACCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCA	61 AGAAACAAGCGGGTGGCTGAGCCAGGCTGTGCACGAGCACCTGACGGGCCCAACAGAC 120 	121 CCATGCTGCATCCAGAGACCTCCCCTGGCGGGGCATCTCCTGGCTGTGCTCCTGGCCC 180	181 TCCTTGGCACCACGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGG 240	241 CCGGAGCCCTGAACAGGAGGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCA 300	301 GCTGGGTCCAGCCCCTGCGGCTGACATGCGGAGGTGGACTGGAGTGACAGCCTGGCCC 360	361 AACTGGCTCAAGCCAGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCC 420	421 TGTGGCGCACCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGGGGCTTGGCGTCCT 480	481 TTGTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGCAGCGGTACAGCCACGCGGCAGGAG 540 	541 AGTGTGCTCGCAACGCCACCTGCACCACTACACGCAGCTCGTGTGGGCCACCTCAAGCC 600	601 AGCTGGGCTGTGGGCGCACCTGTGCTCTGCAGGCCAGACGCGATAGAAGCCTTTGTCT 660 	661 GTGCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGA 720 	721 AGGGTGCCTGGTGTTCGCTCTGCACCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACC 780	781 ATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATG 840 	841 GACGICICAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACT 900	901 GCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGGAGGTGCTCGT 960 	961 GCGTCTGTGACATCGGCGAGGGGGGGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCC 1020
<i>-</i>	QY	Qy Db	QY	QY Db	Oy Op	Oy Db	Qy Db	Qy Db	Qy	Qy	Qy Db	Qy Db	Qy	Oy Db	Qy Db	Qy Db	QQ Dp

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                                                                                                                                              1261 ACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGC 1320
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.021 ACACCTGTGACCTGAGGATCGACGAGACTGCTTCATGGTGTCTTCAGAGGCAGACCCT 1080
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                                           1081 ATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCC
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PLICANT: Baker, Kevin
PLICANT: Botstein, David
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Ferrara, Napoleone Filvaroff, Ellen Gerritsen, Mary

Eaton, Dan

Goddard, Audrey

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                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020150976Alember 30, 1999
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FILING DATE: No. US20020150976Alember 30,
APPLICATION NUMBER: PCT/US99/28301
                                                                                                                                                                                                                                                                          CURRENT PELING DATE: 2001-08-30
PRIOR PAPLICATION NUMBER: 05/09/943,851A
CURRENT PILLING DATE: 2001-08-30
PRIOR PELILNG DATE: 2001-08-30
PRIOR PELILNG DATE: 2001-08-35
PRIOR PELILNG DATE: December 11, 1997
PRIOR FILLING DATE: December 11, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR PELING DATE: PEDUALY 9, 1998
PRIOR PELING DATE: PEDUALY 9, 1999
PRIOR PELING DATE: PEDUALY 10, 1998
PRIOR PELING DATE: PEDUALY 2, 1999
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/2109
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICA
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Godowski, Paul
Grimaldi, Christopher
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                                                                         Hillan,Kenneth
                                                  Gurney, Austin
                                                                                              Kljavin, Ivar
                                                                                                                                           Roy, Margaret
                                                                                                                                                                     Tumas,Daniel
                                                                                                                                                                                              Wood, William
                                                                                                                         Napier, Mary
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        PRIOR FILING DATE: PCCEMENT 17, 2000
PRIOR PELING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/USOU/0414
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: PEDTUARY 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/USOU/08439
PRIOR PILING DATE: March 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR PILING DATE: JUJY 28, 2000
PRIOR PILING DATE: JUJY 28, 2000
PRIOR PILING DATE: JUJY 28, 2000
PRIOR PELING DATE: JUJY 28, 2000
PRIOR PELING DATE: JUJY 28, 2000
PRIOR PELING DATE: PECCHUSOU/2678
PRIOR PELING DATE: PECCHUSOU/6520
PRIOR PELING DATE: FEDTUARY 28, 2001
December 16, 1999
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	AGGCTGCTTCAAAGCCTGGGACC 780 	FICGCAIGAGCTGCCAGAACCAIG 840	CCCTGGCTACACGGGCAGATACT 900 	GTTCCGGAGGAGGAGTGCTCGT 960 	CACCAAGGTGCATTTTCCCTTCC 1020 	GGTGTCTTCAGAGGCAGACACCT 1080 	GGTGCTGGCCCAGATCAAGAGCC 1140 	CCTGGAGACCACCAACGAGGTGA 1200 	GCTCACCTACAAGACCGCCAAGG 1260 	CACCAGTTTTGCCTTTGGGCAGC 1320 	GGGGTTTGGCAACTGCGTGGAGC 1380 	CTGCAAAACCGGTTACA 1440 	CCCAGGGTCCTGAGGCTGACCA 1500 	CITACCTGTCTGCCACCTGTCT 1560 	PAAAGAGGTCTCAGACCTTGCAC 1620 	TIGAGGGCCAGGGAGTGAGTGTT 1680 	AGATGGCTTCAATTAGATGC 1740 	CTCTTCCACCTGCCCAGACCC 1800
	GGCTGCTTCAAAGCCT 	CGCATGAGCTGCCAG 	CCTGGCTACACGGGCA 	TTCCGGGAGGAGGAGTG 	ACCAAGGIGCAITITCO ACCAAGGIGCAITITCO	GTGTCTTCAGAGGCAGA 	GTGCTGGCCCAGATCAA 	CTGGAGACCACCAACGA 	CTCACCTACAAGACCGC 	ACCAGTTTGCCTTTGG 	GGTTTGGCAACTGCGT 	GCAAAACCCGAAACCG 	CAGGGTCCTGAGGCCF 	TACCTGTCTGCCCACC TACCTGTCTGCCCACC	SAGGTCTCAGACCT 	AGGCCAGTGAGGGCCAGGGAGTGA 	FGGGCTTCAATTAG 	TCTTCCACCTGGCCCA

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Sequence 1, Application US/09790264
Patent No. US200200038508A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PRECANASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: 07334-322001
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162 CTGGCTGTGCTCCTGGCCCTCCTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTG 221
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CURRENT FILING DATE: 2001-02-21
PRIOR PAPPLICATION NUMBER: US 09/065,661
PRIOR PELLING DATE: 1998-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR PELLING DATE: 1999-06-22
PRIOR PELLING DATE: 1999-06-22
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR FILING DATE: 1999-07-29
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                    1861 CTGAAAAAAAAAA 1876
                                                                                     Query Match
Best Local Similarity 99.77
Matches 1229; Conservative
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; LOCATION: (95)...(1432)
US-09-790-264-1
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US-09-790-264-1
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US-10-042-141-12
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       CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR PRILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
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Pred. No. 0;
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99.78;
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Matches 1229; Conservative
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US-10-042-141-12
FILE REFERENCE: PZ040P1
                                                                                                                                            SEQ ID NO 12
LENGTH: 1923
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TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: P2040Pl
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-07
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 12
LENGTH: 1923
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Patent No. US20020028449A1
GENERAL INFORMATION:
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Matches 1229; Conservative
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ORGANISM: Homo sapiens
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US-09-726-643-12
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: MCCarthy, Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: 10 USES
TITLE OF INVENTION: 05863
TITLE OF INVENTION: 05863
TITLE OF INVENTION: 0734 -32201
CURRENT APPLICATION NUMBER: US 09/05,661
PRIOR APPLICATION NUMBER: US 09/065,661
PRIOR PELING DATE: 1998-04-23
PRIOR FILING DATE: 1999-06-22
PRIOR PELICATION NUMBER: US 09/065,363
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/337,930
PRIOR FILING DATE: 1999-06-22
PRIOR PELING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/303,630
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/3124,538
PRIOR FILING DATE: 1999-07-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 3, Application US/09790264 Patent No. US20020028508A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-790-264-3
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                GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG
                                                                                                                                       GACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC
GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG
                                                            GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT
                                                                            GCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA
                                                                                                                                                                                                                                                                              781 CAAGTGAGGIGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC
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APPLICANT: Algate, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT PILLIG DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 321, Application US/0988441; Patent No. US20020119158A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(690)
; OTHER INFORMATION: n = A,T,C or G
US-09-884-441-321
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ORGANISM: Homo sapiens
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US-09-884-441-321
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                                 Gaps
                                                                        1 TGGGCTGTGGGCGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTG 60
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0
    Length 690;
                               Indels
Query Match 25.9%; Score 485; DB 10; L
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
Matches 485; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PELING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 53, Application US/09944113 Patent No. US20020156004A1
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
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Hillan, Kenneth
Kljavin, Ivar
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APPLICANT: Botstein, David
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Roy, Margaret
Tumas, Daniel
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US-09-944-413-53
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PRIOR APPLICATION UNDERS: 60/06/335
PRIOR PAPLICATION UNDERS: 60/06/3/278
PRIOR PELING DATE: December 11, 1937
PRIOR PELING DATE: December 11, 1937
PRIOR PLING DATE: December 12, 1937
PRIOR PLING DATE: December 16, 1937
PRIOR PLING DATE: December 18, 1937
PRIOR PLING DATE: December 16, 1998
PRIOR PLING DATE: December 16, 1998
PRIOR PLING DATE: December 16, 1998
PRIOR PLING DATE: December 16, 1999
PRIOR PLING DATE: December 11, 1999
PRIOR PLING DATE: December 13, 2000
PRIOR PRING DATE: December 13, 2000
PRIOR PRING DATE: December 13, 2000
PRIOR PLING DATE: PEDULARY 22, 2000
PRIOR PLING DATE: PEDULARY 22, 2000
PRIOR PLING DATE: DECEMBER: PC70800/3659
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PRIOR PLING DATE
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RESULT 23
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CURRENT APPLICATION NUMBER: US/09/866,028

PRIOR APPLICATION NUMBER: 00/067,411

PRIOR PELING DATE: December 11, 1997

PRIOR PELING DATE: December 12, 1997

PRIOR PELING DATE: December 16, 1997

PRIOR PELING DATE: December 17, 1997

PRIOR PELING DATE: DECEMBER: 60/069, 873

PRIOR PELING DATE: DECEMBER: 60/069, 873

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PRIOR PELING DATE: DECEMBER: 60/069, 873
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                                                                               ; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-413-53
                                                                                                                                                                                        Query Match 2.4%; Score 45; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 45; Conservative 0; Mismatches
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FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/068,017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/074,086
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Grimaldi, Christopher
                                                 ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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LENGTH: 45
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PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PULING DATE: December 12, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR FILING DATE: MATCH 3, 1999
PRIOR FILING DATE: MATCH 3, 1999
PRIOR PELING DATE: MATCH 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: September 15, 1999
PRIOR PELING DATE: No. US20020165143Alember 30, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: PECT/US99/28301
PRIOR FILING DATE: PECT/US99/28301
PRIOR FILING DATE: PECT/US99/28301
PRIOR FILING DATE: PECMENT 11, 2000
PRIOR FILING DATE: FEBURATY 22, 2000
PRIOR FILING DATE: FEBURATY 22, 2000
PRIOR PELING DATE: FEBURATY 23, 2000
PRIOR PELING DATE: PECT/US00/05841
PRIOR PELING DATE: MATCH 30, 2000
PRIOR PELING DATE: MAY 22, 2000
PRIOR PELING DATE: MAY 23, 2000
PRIOR PELING DATE: MAY 23, 2000
PRIOR PELING DATE: MAY 28, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/2578
PRIOR FILING DATE: DECEMBER: PCT/US00/2520
PRIOR FILING DATE: PEDULATY 28, 2001
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                                                                                                                                                                              FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
                                                                                                                                                                                                                                                      FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
                                                                    PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR FILING DATE: JULY 28, 1999
PRIOR FILING DATE: September: 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/1933
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
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APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Mapoleone
APPLICANT: Filvaroff, Ellen
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LENGTH: 45
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT APPLICATION NUMBER: US/09/966,028
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020168715Alember 30, 1999
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FILING DATE: NO. US20020168715Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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June 22, 1999
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PRIOR FILING DATE: December 16, 1997
PRIOR PELICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR PELICATION NUMBER: 60/069,702
PRIOR PELICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 17, 1997
PRIOR PELING DATE: December 18, 1997
PRIOR PELING DATE: December 18, 1997
PRIOR PELING DATE: December 18, 1997
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: PEDRUARY 9, 1998
PRIOR PELING DATE: FEBRUARY 9, 1998
PRIOR PELING DATE: FEBRUARY 9, 1998
PRIOR PELING DATE: FEBRUARY 9, 1998
PRIOR PELING DATE: PEBRUARY 9, 1998
PRIOR PELING DATE: PEBRUARY 9, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: DECEMBER 10, 1999
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APPLICATION NUMBER: 60/069,696
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Godowski, Paul
Grimaldi, Christopher
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                                                                     Gurney, Austin
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Tumas, Daniel
Wood, William
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CURRENT APPLICATION NUMBER: US/09/944,944

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: December 3, 1997

PRIOR FILING DATE: December 3, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069335
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              PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: February 1, 2000
PRIOR FILING DATE: February 1, 2000
PRIOR FILING DATE: February 2, 2000
PRIOR FILING DATE: February 2, 2000
PRIOR FILING DATE: February 2, 2000
PRIOR PLING DATE: March 2, 2000
PRIOR PLING DATE: March 3, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR PRILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDIUS 1, 2001
PRIOR FILING DATE: FEBRUARY 28, 2001
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
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Patent No. US20020173463A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Napier, Mary
Roy, Margaret
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LENGTH: 45
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APPLICANT:
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OR FILING DATE: December 1, 1998

OR APPLICATION NUMBER: 09/216,021

OR FILING DATE: December 16, 1998

OR RILING DATE: December 22, 1998

OR APPLICATION NUMBER: 09/218,517

OR FILING DATE: December 22, 1998

OR APPLICATION NUMBER: 09/254,311

OR RELING DATE: March 3, 1999

OR APPLICATION NUMBER: PCT/US99/1252

OR RAPLICATION NUMBER: PCT/US99/21090

OR RILING DATE: September 15, 1999

OR APPLICATION NUMBER: PCT/US99/28409

OR RELING DATE: NO. US20020173463ALember 30, 1999

OR RELING DATE: NO. US20020173463ALember 30, 1999

OR RILING DATE: NO. US20020173463ALember 30, 1999

OR RILING DATE: NO. US20020173463ALember 30, 1999

OR RILING DATE: December1, 1999
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PRIOR PELICATION NUMBER: 60/146,222
PRIOR PELICATION NUMBER: 60/146,222
PRIOR PELICATION NUMBER: 60/146,222
PRIOR PELING DATE: September 16, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 17, 1998
PRIOR PELING DATE: December 17, 1998
PRIOR PELING DATE: December 12, 1998
PRIOR PELING DATE: December 22, 1999
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PRIOR PELING DATE: PEROTYGS99/28199
PRIOR PELING DATE: PEPUSON NUMBER: PCT/US99/2813
PRIOR PELING DATE: DECEMBER 1, 1999
PRIOR PELING DATE: PEPUSON NUMBER: PCT/US99/28101
PRIOR PELING DATE: PEPUSON POLOSON PRIOR PELING DATE: MATC 2, 2000
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R RAPLICATION NUMBER: 60/112,850
R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 60/113,296
RR FILING DATE: December 22, 1998
R APPLICATION NUMBER: 60/146,222
RR FILING DATE: 301y 28, 1999
R FILING DATE: SEPTEMBER: PCT/VCS9/1930
R FILING DATE: SEPTEMBER: PCT/VCS9/1930
R FILING DATE: SEPTEMBER: PCT/VCS9/1930
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: December 18, 1997
APPLICATION UNMBER: 60/070,440
FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
                                                                                                                                                                    FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
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APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
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                                   FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
                                                                                                  FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
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APPLICATION NUMBER: 60/068,017
APPLICATION NUMBER: 60/069,696
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
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2.4%; Score 45; DB 9; Length 45; 100.0%; Pred. No. 1.8e-10; Live 0; Mismatches 0; Indels
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                                                                         1254 GCCAAGGACTCCTTCCGCTGGGCCACAGGGGGAGCACCAGGCCTTC 1298
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Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    Sequence 53, Application US/09866028 Patent No. US20020058309A1 GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Filvaroff, Ellen
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Kljavin, Ivar
Napier, Mary
                                    45; Conservative
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Godowski, Paul
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Tumas, Daniel
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                 Best Local Similarity
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US-09-866-028-53
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APPLICANT
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HILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC HILE OF INVENTION: ACIDS ENCODING THE SAME
     FILING DATE: February 11, 2000 APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                                      FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
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APPLICANT: WOOD, William:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 06/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,349
PRIOR APPLICATION NUMBER: 60/069,369
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
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Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0;
                         PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR PILING DATE: Execember 1, 2000
PRIOR PILING DATE: February 28, 2001
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
APPLICATION NUMBER: PCT/US00/08439
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APPLICATION NUMBER: 60/069,702
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Grimaldi,Christopher
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Hillan, Kenneth
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Roy, Margaret
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LENGTH: 45
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1 CURRENT APPLICATION NUMBER: US/09/945,587 CURRENT FILING DATE: 2001-09-26 PRIOR APPLICATION NUMBER: 09/866,028 PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: December 1, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1998
PRIOR FILING DATE: FEBRUARY 9, 1998
PRIOR FILING DATE: FEBRUARY 9, 1998
PRIOR FILING DATE: PEBRUARY 9, 1998
PRIOR FILING DATE: PEBRUARY 25, 1998
PRIOR FILING DATE: PEBRUARY 25, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: SEPTUARY 25, 1998
PRIOR FILING DATE: December 16, 1998
                                                                                                                         Sequence 53, Application US/09945587 Patent No. US20020127643A1
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Grimaldi, Christopher
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APPLICANT: Botstein, David
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0;
                                                                               PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR PLILING DATE: December 18, 1997
PRIOR PLILING DATE: December 18, 1997
PRIOR PLILING DATE: December 19, 1998
PRIOR PLILING DATE: February 9, 1998
PRIOR PLILING DATE: February 9, 1998
PRIOR PLILING DATE: February 9, 1998
PRIOR PLILING DATE: February 25, 1998
PRIOR PLILING DATE: February 25, 1998
PRIOR PLILING DATE: Pebruary 25, 1998
PRIOR PLILING DATE: December 16, 1998
PRIOR PLILING DATE: December 22, 1998
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PRIOR PLILING DATE: PEDVINGATION NUMBER: PCT/US99/28301
PRIOR PLILING DATE: PEDVINGATION NUMBER: PCT/US00/08419
PRIOR PRILING DATE: PEDVINGATION NUMBER: PCT/US00/08419
PRIOR PRILING DATE: PEDVINGATION NUMBER: PCT/US00/08419
PRIOR PRILING 
                        APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
FILING DATE: December 17,
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ORGANISM: Artificial Sequence
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FILING DATE: No. US2002013276BAlember 30, 1999 APPLICATION NUMBER: PCT/US99/28313
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DR APPLICATION NUMBER: 60/112,850
DR FILING DATE: December 16, 1998
DR APPLICATION NUMBER: 60/113,296
DR FILING DATE: December 22, 1998
DR FILING DATE: December 22, 1998
DR FILING DATE: July 28, 1999
DR FILING DATE: July 28, 1999
DR APPLICATION NUMBER: PCT/US98/19330
              CURRENT APPLICATION NUMBER: US/09/945,015
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APPLICATION NUMBER: PCT/US00/20710
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FILING DATE: September 15, 1999
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APPLICATION NUMBER: PCT/US98/25108
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FILING DATE: June 22, 1999
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PRIOR FILING DATE: No. 117777777
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APPLICATION NUMBER: PCI/US99/30095
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APPLICATION NUMBER: PCT/USOO/05841
FILING DATE: March 2, 2000
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FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
                                                     PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: 06/069,334
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: Eberuary 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: PEDRUARY 25, 1998
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APPLICATION UNMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
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                                                                                                                                                          FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US2002012/643Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US2002012/643Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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PRIOR PLING DATE: December1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR PLING DATE: December 16, 1999
PRIOR PELING DATE: December 16, 1999
PRIOR PELING DATE: February 11, 2000
PRIOR PELING DATE: February 11, 2000
PRIOR PLING DATE: PEDRORUALY 22, 2000
PRIOR PLING DATE: PEDRORUALY 23, 2000
PRIOR PLING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: MAY 22, 2000
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
                                                                                                                 FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US00/32678
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
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Matches 45; Conservative
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Hillan, Kenneth
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LENGTH: 45
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CURRENT APPLICATION NUMBER: US/09/966,028

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: Docember 3, 1997

PRIOR FILING DATE: Docember 11, 1997

PRIOR PLING DATE: Docember 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR PLING DATE: Docember 12, 1997

PRIOR PLING DATE: Docember 12, 1997

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PRIOR APPLICATION NUMBER: 60/069,696
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                  PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 53
LENGTH: 45
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""FLICATION NUMBER: 60/069,694

"KIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 16, 10°-

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APPLICATION NUMBER: 60/069,873
FILLING DATE: December 17, 1997
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FILING DATE: December 18, 1997
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Grimaldi, Christopher
PRIOR FILING DATE: July 28, 2000
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APPLICANT: Botstein, David
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Tumas, Daniel
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US-09-944-996-53
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020132981Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020132981Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR PELING DATE: March 2, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: MARCH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/1404
PRIOR FILING DATE: MAY 22, 2000
PRIOR PRILING DATE: JULY 28, 2000
PRIOR PRILING DATE: JULY 28, 2000
PRIOR PRILING DATE: JULY 28, 2000
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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                               PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: FEBRUARY 9, 1998
PRIOR FILING DATE: FEBRUARY 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR APPLICATION NUMBER: 60/112,296
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: DECEMBER: 22, 1998
FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
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Best Local Similarity 100.0
Matches 45; Conservative
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US-09-944-097-53
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LENGTH: 45
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APPLICATION NUMBER: PCT/US99/28409
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LENGTH: 45
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APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/944,097
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/069,334
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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PPLICATION NUMBER: 09/254,311
FILING DATE: MARCH 3, 1999
APPLICATION NUMBER: PCT/US99/12252
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FILING DATE: September 15, 1999
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PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR RILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR RILING DATE: December 12, 1997
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PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/074,092
FILING DATE: February 9, 1998
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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FILING DATE: February 25, 1998
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APPLICATION NUMBER: 09/218,517
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APPLICATION NUMBER: 60/069,873
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APPLICATION NUMBER: 60/068,017
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Grimaldi, Christopher
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                                                                                                          Ferrara, Napoleone
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                                            APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Hillan, Kenneth
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                                                                                                                                                       Gerritsen, Mary
US20020133675A1
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Tumas, Daniel
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILING DATE: No. US20020133675Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020133675Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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                                                                        PRIOR FILLING DATE: NO. US.CUCAGL3307.0341eminet.
PRIOR FILLING DATE: December1, 1999
PRIOR FILLING DATE: December1, 1999
PRIOR FILLING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILLING DATE: PEbruary 11, 2000
PRIOR FILLING DATE: February 22, 2000
PRIOR FILLING DATE: Rebruary 22, 2000
PRIOR FILLING DATE: March 30, 2000
PRIOR FILLING DATE: July 28, 2000
PRIOR FILLING DATE: July 28, 2000
PRIOR FILLING DATE: DECEMBER: PCT/US00/32678
PRIOR FILLING DATE: DECEMBER: PCT/US00/32678
PRIOR FILLING DATE: PEDRUARY 28, 2001
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CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: 06/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
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Patent No. US20020142419A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
Gerritsen, Mary
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45; Conservative
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APPLICANT: Botstein, David
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Kljavin, Ivar
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PRIOR PELLOR DELE DECEMBE 11, 1997
PRIOR PELLOR NUMBER: 60/069,278
PRIOR PELLOR MUNBER: 60/069,278
PRIOR PELLOR MUNBER: 60/069,28
PRIOR PELLOR MUNBER: 60/069,68
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PRIOR PELLOR MUNBER: 60/069,68
PRIOR APPLICATION NUMBER: 60/069,68
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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                                                                                                                                                    ; OTHER INFORMATION: Synthetic oligonucleotide probe US-09-944-432-53
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PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILLING DATE: December 17, 1997
PRIOR FILLING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILLING DATE: December 18, 1997
PRIOR FILLING DATE: January 5, 1998
PRIOR FILLING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
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                              TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Hillan, Kenneth
Kljavin, Ivar
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APPLICANT: Botstein, David
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Tumas, Daniel
Wood, William
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US-09-943-762-53
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LENGTH: 45
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILING DATE: No. US20020142959Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020142959Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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CURRENT APPLICATION NUMBER: US/09/94,654
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-25
PRIOR PELICATION NUMBER: 09/866,028
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PELING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR PILING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
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PRIOR PELING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR PELING DATE: December 17, 1997
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PRIOR PELICATION NUMBER: 60/069,870
PRIOR PELING DATE: December 17, 1997
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RAPPLICATION UNUBER: 09/218,517
RAPLICATION NUMBER: 09/254,311
RAPLICATION NUMBER: 09/254,311
R FILING DATE: MARCH 3, 1999
R APPLICATION NUMBER: PCT/US99/1252
R FILING DATE: June 22, 1999
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
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APPLICATION WUMBER: 60/070, 945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
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APPLICATION NUMBER: 09/216,021
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APPLICATION NUMBER: 60/068,017
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Grimaldi, Christopher
Gurney, Austin
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Tumas,Daniel
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PRIOR FILLING DATE: JUNE 22, 1999

PRIOR FILLING DATE: JUNE 22, 1999

PRIOR FILLING DATE: JUNE 22, 1999

PRIOR FILLING DATE: September 15, 1999

PRIOR FILLING DATE: September 15, 1999

PRIOR FILLING DATE: No. US20020142958Alember 30, 1999

PRIOR PELLING DATE: No. US20020142958Alember 30, 1999

PRIOR PELLING DATE: No. US20020142958Alember 30, 1999

PRIOR FILLING DATE: No. US20020142958Alember 30, 1999

PRIOR FILLING DATE: December1, 1999

PRIOR FILLING DATE: December1, 1999

PRIOR FILLING DATE: PECTUARY 11, 2000

PRIOR PRICATION NUMBER: PCT/US00/04414

PRIOR FILLING DATE: FEBRUARY 21, 2000

PRIOR FILLING DATE: FEBRUARY 22, 2000

PRIOR FILLING DATE: FEBRUARY 22, 2000

PRIOR FILLING DATE: FEBRUARY 22, 2000

PRIOR FILLING DATE: MATCH 30, 2000

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PRIOR FILLING DATE: MATCH 30, 2000

PRIOR FILLING DATE: MAY 22, 2000

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DR FILING DATE: February 25, 1998
DR APPLICATION NUMBER: 60/112,850
DR PILING DATE: December 16, 1998
DR APPLICATION NUMBER: 60/113,296
DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 60/146,222
DR FILING DATE: July 28, 1999
DR APPLICATION NUMBER: CDT/US98/19330
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US01/06520
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 53
LENGTH: 45
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Patent No. US20020142959A1
GENERAL INFORMATION:
APPLICANT: Batker, Kevin
APPLICANT: Botstein, David
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Ferrara,Napoleone
Filvaroff,Ellen
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US-09-944-654-53
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020150976A1ember 30, 1999
FILING DATE: No. US20020150976A1ember 30, 1999
FILING DATE: No. US20020150976A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
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PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 53
LENGTH: 45
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APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
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APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
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R APPLICATION NUMBER: 60/074,086
F PILING DATE: February 9, 1998
R PRILICATION NUMBER: 60/074,092
R FILING DATE: February 9, 1998
R APPLICATION NUMBER: 60/075,945
R FILING DATE: February 25, 1998
R APPLICATION NUMBER: 60/112,850
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FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 2, 1998
APPLICATION NUMBER: 60/146,222
APPLICATION NUMBER: 60/069,425
                                       APPLICATION NUMBER: 60/069,696
                                                            FILLING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
                                                                                                 FILING DATE: December 16, 1997
APPLICATION UNMARR: 60//069,70,
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,87,
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CURRENT APPLICATION NUMBER: US/09/943,851A
CURRENT FILING DATE: 2001-06-30
PRIOR APPLICATION NUMBER: US/09/866,028
PRIOR FILING DATE: DCCOMDer: 3, 1997
PRIOR FILING DATE: DCCOMDer: 3, 1997
PRIOR FILING DATE: DCCOMDer: 11, 1997
PRIOR FILING DATE: DCCOMDer: 11, 1997
PRIOR APPLICATION NUMBER: 60/669,334
PRIOR FILING DATE: DCCOMDer: 11, 1997
PRIOR PELICNE DATE: DCCOMDER: 60/669,335
PRIOR APPLICATION NUMBER: 60/669,335
PRIOR APPLICATION NUMBER: 60/669,378
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; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-654-53
               PRIOR FILING DATE: DECEMBER: FOT/US99/30095
PRIOR FILING DATE: DECEMBER: FOT/US99/30095
PRIOR APPLICATION NUMBER: FOT/US00/03565
PRIOR FILING DATE: FEBTUARY 11, 2000
PRIOR PLING DATE: FEBTUARY 22, 2000
PRIOR FILING DATE: FEBTUARY 22, 2000
PRIOR FILING DATE: MAICH 2, 2000
PRIOR FILING DATE: MAICH 2, 2000
PRIOR PLICATION NUMBER: PCT/US00/O8419
PRIOR APPLICATION NUMBER: PCT/US00/1404
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: PCT/US00/3678
PRIOR FILING DATE: DECEMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: EEDLUARY 28, 2001
NUMBER: PCT/US01/06520
PRIOR FILING DATE: FEDLUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
  FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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Kljavin, Ivar
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Botstein, David
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Godowski, Paul
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Tumas, Daniel
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LENGTH: 45
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/1930
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: PCT/USS92/30095
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
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PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR APPLICATION NUMBER: 60/116,222
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PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR FILING DATE: February 9, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/216,021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING DATE: December 1,
                                                                                     Roy,Margaret
                                                                                                         Tumas, Daniel
                                                                                                                               Wood, William
                                                        Napier, Mary
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APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: 07334-322001
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100.0%; Pred. No. 0.00076;
                                                2.4%; Score 45; DB 10; I 100.0%; Pred. No. 1.8e-10; ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/790,264
CURRENT FILING DATE: 2001-02-21
PRIOR FULING DATE: 2001-02-21
PRIOR PELLING DATE: 1998-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-06-22
PRIOR PELLING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1999-06-22
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09790264
Patent No. US20020028508A1
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Goddward, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
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Filvaroff, Ellen
                                           Query Match
Best Local Similarity 100.
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eaton, Dan
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US-09-944-413-103/c
                                                                                                                                                                                                                                                           RESULT 36
US-09-790-264-5/c
US-09-943-851A-53
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LENGTH: 30
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/944,413

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/066,741

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR FILING DATE: December 12, 1997

PRIOR FILING DATE: December 12, 1997

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR APPLICATION NUMBER: 60/069,702
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FILING DATE: NO. US20020156004Alember 30, 1999
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ING DATE: No. US20020156004Alember 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE LINE DATE: December 16, 1998

DR APPLICATION NUMBER: 09/218, 517

PR FILING DATE: December 22, 1998

DR APPLICATION NUMBER: 09/254, 311

DR FILING DATE: March 3, 1999

DR APPLICATION NUMBER: 02/1999

DR APPLICATION NUMBER: 02, 1999

DR APPLICATION NUMBER: 02, 1999
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LENGTH:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
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100.0%; Pred. No. 0.016;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic oligonucleotide probe US-09-944-413-103
             FRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR PAPLICATION NUMBER: PCT/USO0/05841
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDT/USO0/26520
PRIOR FILING DATE: PEDT/USO1/06520
APPLICATION NUMBER: PCT/US00/04414
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PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 3, 1997
PRIOR PELLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR PRILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
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PRIOR FILLING DATE: 2001-05-25
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Patent No. US20020165143A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
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Best Local Similarity 100.C
Matches 27; Conservative
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APPLICANT: Botstein, David
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Goddard, Audrey
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Roy, Margaret
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: July 28, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999/254,311
PRIOR FILING DATE: March 3, 1999/254,311
PRIOR FILING DATE: September 12, 1999
PRIOR FILING DATE: NO. US20020165143Alember 30, 1999
PRIOR FILING DATE: NO. US20020165143Alember 30, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: DECEMBER: PCT/US99/30055
PRIOR FILING DATE: DECEMBER: PCT/US99/30056
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PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR PILING DATE: MAICH 2, 2000
PRIOR PELING DATE: MAICH 30, 2000
PRIOR FILING DATE: MAICH 30, 2000
PRIOR PILING DATE: MAY 22, 2000
PRIOR PELING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 23, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: DECEMBER : PCT/USO0/32678
PRIOR FILING DATE: DECEMBER IN 2000
PRIOR FILING DATE: DECEMBER IN 2000
PRIOR FILING DATE: EDECEMBER IN 2000
PRIOR FILING DATE: FEBRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December 22, 1998 APPLICATION NUMBER: 60/146,222 FILING DATE: July 28, 1999
                                                                                                                                                                                                                                                      FILING DATE: December 18, 1997 APPLICATION NUMBER: 60/070,440
                                                                                                                                                                                                                                                                                                                               FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
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                                     FILLING DATE: December 16, 1997 APPLICATION NUMBER: 60/069,870
APPLICATION NUMBER: 60/069,702
                                                                                                                                                                                  FILING DATE: December 17, 1997 APPLICATION NUMBER: 60/068,017
                                                                                                                                            APPLICATION NUMBER: 60/069,87
                                                                                                          FILING DATE: December 17,
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Gaps

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IITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC IITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR FULING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR PLICATION NUMBER: 60/069335
PRIOR PLICATION NUMBER: 60/069,378
PRIOR PELICATION NUMBER: 60/069,278
PRIOR PELICATION NUMBER: 60/069,425
PRIOR PELICATION NUMBER: 60/069,425
PRIOR PELICATION NUMBER: 60/069,694
PRIOR PILING DATE: DECEMBER 11, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR PILING DATE: DECEMBER 16, 1997
PRIOR PILING DATE: DECEMBER 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR PILING DATE: DECEMBER 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR PILING DATE: DECEMBER 11, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR APPLICATION NUMBER: 60/069,070
PRIOR PILING DATE: DECEMBER 17, 1997
PRIOR PELING DATE: DECEMBER 17, 1997
PRIOR PELING DATE: DECEMBER 19, 1997
PRIOR APPLICATION NUMBER: 60/0704,086
PRIOR PILING DATE: DECEMBER 19, 1998
PRIOR PILING DATE: TEBLUARY 9, 1998
PRIOR PILING DATE: FEBLUARY 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
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                         27 TGGGAAGATGGCCTTCAATTAGATGGC 1
                                                                                                                                                                                                                Sequence 103, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: 09/216,021
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Grimaldi, Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
Kljavin, Ivar
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APPLICANT: Botstein, David
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR PRILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PRILING DATE: No. US20020168715Alember 30, 1999
PRIOR PRILING DATE: No. US20020168715Alember 30, 1999
PRIOR PRILING DATE: December 15, 09/05/21090
PRIOR PRILING DATE: December 15, 1999
PRIOR PRILING DATE: December 17, 09/05/21090
PRIOR PRILING DATE: December 17, 09/05/21090
PRIOR PRILING DATE: December 17, 09/05/21090
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PRIOR PELLORION NUMBER: PCT/USS9/30055
PRIOR FILING DATE: December 16, 1999
PRIOR PELLORION NUMBER: PCT/USS00/03565
PRIOR PILING DATE: February 11, 2000
PRIOR PELLORION NUMBER: PCT/USS00/0414
PRIOR FILING DATE: February 22, 2000
PRIOR PLING DATE: February 22, 2000
PRIOR PLING DATE: March 2, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PELLING DATE: May 22, 2000
PRIOR PELLING DATE: May 22, 2000
PRIOR PELLING DATE: July 28, 2000
PRIOR PELLING DATE: July 28, 2000
PRIOR PELLING DATE: July 28, 2000
PRIOR PELING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USS0/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USS0/3600
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Patent No. US20020173463A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Matches 27; Conservative
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Napier, Mary
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LENGTH: 27
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FILING DATE: NO. US20020173463Alember 30, 1999 APPLICATION NUMBER: PCT/US99/28313 FILING DATE: NO. US20020173463Alember 30, 1999 APPLICATION NUMBER: PCT/US99/28301 FILE REFERENCY: P.239 PLCI.
CURRENT PELLING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/06/411
PRIOR PILING DATE: December 3, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR PILING DATE: December 17, 1997 ACIDS ENCODING THE SAME FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999 PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03555
PRIOR FILING DATE: FEBRUARY 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000 APPLICATION NUMBER: PCT/US98/19330 FILING DATE: September 16, 1998 APPLICATION NUMBER: PCT/US98/25108 FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/USO0/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/USO0/14042 FILING DATE: September 15, 1999 APPLICATION NUMBER: PCT/US99/28409 FILING DATE: February 22, 2000 APPLICATION NUMBER: PCT/US00/05841 APPLICATION NUMBER: PCT/US99/21090 FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945 APPLICATION NUMBER: 09/216,021 FILING DATE: December 16, 1998 APPLICATION NUMBER: 09/218,517 FILING DATE: December 22, 1998 APPLICATION NUMBER: 60/146,222 FILING DATE: February 25, 1998 APPLICATION NUMBER: 60/112,850 FILING DATE: December 16, 1998 APPLICATION NUMBER: 60/113,296 FILING DATE: July 28, 1999 FILING DATE: December1, December 1 FILE REFERENCE: P2548P1C1 TITLE OF INVENTION: FILING DATE: FILING DATE: PRIOR RIOR PRIOR PRIOR PRIOR RIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

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CURRENT APPLICATION NUMBER: US/09/866,028
Prior addlication Partication Part
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION UNBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: FEBRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 103
LENGTH: 27
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US-09-944-449-103/c
; Sequence 103, Application US/09944449
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Gurney, Austin
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APPLICANT: Botstein, David
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Goddard, Audrey
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LENGTH: 27
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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/944,449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069335
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APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
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R APPLICATION NUMBER: 60/112,850
R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 60/113,296
R FILING DATE: December 22, 1998
RR APPLICATION NUMBER: 60/146,222
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APPLICATION NUMBER: 60/069,278
FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,428
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APPLICATION WUMBER: 60/066,870
FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/069,873
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APPLICATION WUMBER: 60/070,440
ELING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/069,702
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APPLICATION NUMBER: 60/075,945
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APPLICATION NUMBER: 09/216,021
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APPLICATION NUMBER: 09/218,517
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APPLICATION NUMBER: 60/068,017
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Grimaldi, Christopher
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                                                                                                Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
                                        Botstein, David
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Hillan, Kenneth
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Patent No. US20020102647A1
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Tumas, Daniel
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US99/3005
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
                      FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020102647Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
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100.0%; Pred. No. 0.016;
tive 0; Mismatches 0
                                                                   PRIOR FILING DATE: NO. US20020102647Alember 3
PRIOR PELING DATE: DECEMBER! PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/380095
PRIOR FILING DATE: DECEMBER 16, 1999
PRIOR FILING DATE: DECEMBER 16, 1999
PRIOR FILING DATE: PEDRUARY 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: MARCH 2, 2000
PRIOR PILING DATE: MARCH 2, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR PELING DATE: MAY 22, 2000
PRIOR PILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER 1, 2000
PRIOR FILING DATE: PEDRUARY 28, 2001
PRIOR PILING DATE: PEDRUARY 28, 2001
PRIOR FILING DATE: PEDRUARY 28, 2001
PRIOR FILING DATE: PEDRUARY 28, 2001
PRIOR PRIOR PILING DATE: PEDRUARY 28, 2001
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
APPLICATION NUMBER: PCT/US99/21090
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; Patent No. US20020110859A1
; GENERAL INFORMATION:
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Gurney, Austin
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
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APPLICANT: Botstein, David
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Napier, Mary
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Best Local Similarity
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FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/VS99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/2813
FILING DATE: NO. US20020110859Alember 30, 1999
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APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US0/20710
FILING DATE: July 28, 2000
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FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
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APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
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APPLICATION NUMBER: PCT/US98/25108
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
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APPLICATION NUMBER: PCT/USO0/03565
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FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/USOO/08439
FILING DATE: March 30, 2000
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APPLICATION NUMBER: PCT/US00/04414
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                                                                                                                         R FILING DATE: December 11, 1997
R APPLICATION NUMBER: 60/069,425
R FILING DATE: December 12, 1997
R APPLICATION NUMBER: 60/069,696
R FILING DATE: December 16, 1997
R APPLICATION NUMBER: 60/069,694
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APPLICATION NUMBER: 60/069, 870
ILING DATE: December 17
SPILTANTON
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APPLICATION UNDBER: 60/060,873
FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/112,850
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APPLICATION NUMBER: 60/110, 296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146, 222
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
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APPLICATION NUMBER: 60/069,334 FILING DATE: December 11, 1997 APPLICATION NUMBER: 60/06935 FILING DATE: December 11, 1997
                                                                                                    APPLICATION NUMBER: 60/069,278
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2544B1C1.

CURRENT APPLICATION NUMBER: US/09/945,587

CURRENT FILING DATE: 2001-09-26

PRIOR PLICATION NUMBER: 60/866,028

PRIOR PLICATION NUMBER: 60/866,028

PRIOR PLICATION NUMBER: 60/067,411

PRIOR PLICATION NUMBER: 60/067,411

PRIOR PLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR PLICATION NUMBER: 60/069,278

PRIOR PLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 12, 1997

PRIOR PLICATION NUMBER: 60/069,425

PRIOR PLICATION NUMBER: 60/069,425

PRIOR PLICATION NUMBER: 60/069,425

PRIOR PLICATION NUMBER: 60/069,425

PRIOR PLILING DATE: December 12, 1997

PRIOR PLILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,696
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1.4%; Score 27; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                              ; OTHER INFORMATION: Synthetic oligonucleotide probe US-09-944-457-103
                                                                                                                                                                                                                                                                                                        1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/069,694
RILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 103, Application US/09945587 Patent No. US20020127643A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December 16, 1997 APPLICATION NUMBER: 60/069,870
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APPLICATION NUMBER: 60/068,017
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Grimaldi, Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                                                                                            ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 120
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Napier, Mary
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Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                      SEQ ID NO 103
LENGTH: 27
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APPLICANT:
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                                                                        TYPE: DNA
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APPLICANT: WOOD WILLiam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 1998
APPLICATION NUMBER: 09/218,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
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APPLICATION NUMBER: 60/069,702
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APPLICATION NUMBER: 60/075,945
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APPLICATION UNDRER: 60/112, 850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113, 296
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
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PRIOR APPLICATION NUMBER: 60/069,694
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APPLICATION NUMBER: 60/069,87
FILING DATE: December 17, 199
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      Ferrara, Napoleone
                                   Filvaroff, Ellen
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Hillan, Kenneth
                                                                 Gerritsen, Mary
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Napier, Mary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR APPLICATION NUMBER: PCT/US99/12252
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR FILING DATE: No. US20020127643Aamber 30, 1999
OR RAPLICATION NUMBER: PCT/US99/28313
OR RAPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: No. US20020127643Aamber 30, 1999
OR FILING DATE: No. US20020127643Aamber 30, 1999
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                                                                          PRIOR APPLICATION NUMBER: 60/112,856
PRIOR APPLICATION NUMBER: 60/112,856
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28109
PRIOR FILING DATE: December 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28109
PRIOR FILING DATE: December 15, 1999
PRIOR FILING DATE: December 15, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR PRILING DATE: December 16, 1999
PRIOR PRILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR PRILICATION NUMBER: PCT/US99/28009
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: DECEMBER PCT/US09/04414
PRIOR FILING DATE: DECEMBER PCT/US09/04414
PRIOR FILING DATE: PEDTUARY 22, 2000
PRIOR FILING DATE: MATCH 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: MATCH 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: MATCH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: MATCH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PRILING DATE: JULY 28, 2000
PRIOR PRILING DATE: JULY 28, 2001
PRIOR PRILING DATE: PCDTUARY 28, 2001
PRIOR PRILING DATE: PCDTUARY 28, 2001
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                                                    R FILING DATE: February 25, 1998
R APPLICATION NUMBER: 60/112,850
R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 60/113,296
R FILING DATE: December 22, 1998
R APPLICATION NUMBER: 60/146,222
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Patent No. US20020132768A1
GENERAL INFORMATION: APPLICAMT: Baker, Kevin
APPLICAMT: Botstein, David
APPLICAMT: Eaton, Dan
FILING DATE: February 9, 1998
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US-09-945-015-103/c
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LENGTH: 27
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TYPE: DNA

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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020132768Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313

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TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 103
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FILING DATE: No. US20020132768Alember 30, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic oligonucleotide probe US-09-945-015-103
          PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: Docember1, 1999
PRIOR FILING DATE: Docember1, 1999
PRIOR FILING DATE: Docember 16, 1999
PRIOR FILING DATE: Docember 16, 1999
PRIOR FILING DATE: PEDFUATY 11, 2000
PRIOR PILING DATE: FEBTUARY 22, 2000
PRIOR PELING DATE: FEBTUARY 22, 2000
PRIOR PELING DATE: FEBTUARY 22, 2000
PRIOR PELING DATE: PEDTUARY 23, 2000
PRIOR PELING DATE: MARCH 2, 2000
PRIOR PELING DATE: MARCH 30, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR PILING DATE: DOCEMBER: PCT/US00/20710
PRIOR PILING DATE: DOCEMBER: PCT/US00/32678
PRIOR FILING DATE: DOCEMBER: PCT/US01/06520
PRIOR FILING DATE: PEDTUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
LENGTH: 27
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CURRENT APPLICATION NUMBER: U5/09/944,396
CURRENT FILING DATE: 2001-09-26
PRIOR PEPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
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Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
Gerritsen, Mary
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Napier, Mary
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Best Local Similarity
Matches 27; Conserva
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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020132981A1ember 30, 1999
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FILING DATE: No. US20020132981Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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PRIOR PPLICATION NUMBER: 09/254 311
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR PLING DATE: SEPTEMBER 15, 1999
PRIOR PELING DATE: NO. US20020132981A1ember PRIOR PRING DATE: NO. US20020132981A1ember PRIOR PLING DATE: DECEMBER: PCT/US99/28301
PRIOR FILING DATE: DECEMBER: PCT/US99/3095
PRIOR PLING DATE: DECEMBER: PCT/US99/3095
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR PLING DATE: FEBRUARY 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR PLING DATE: FEBRUARY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR PLING DATE: MATCH 30, 2000
PRIOR PLING DATE: MATCH 30, 2000
PRIOR PLING DATE: MAY 22, 2000
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OR APPLICATION NUMBER: 09/218,517
OR PILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/1255
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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PRIOR APPLICATION NUMBER: PCT/US01/06520
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APPLICATION NUMBER: 60/070,440
APPLICATION NUMBER: 60/074,086
APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/074,092
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                                                                                                     FILING DATE: December 12, 1997 APPLICATION NUMBER: 60/069,696
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APPLICATION NUMBER: 60/069,278
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APPLICATION UNDBER: 60/069,694
APPLICATION NUMBER: 60/069,702
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                                                                  APPLICATION NUMBER: 60/069,425
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CURRENT APPLICATION NUMBER: US/08/66,028

PRIOR FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 12, 1997

PRIOR FILING DATE: December 12, 1997

PRIOR FILING DATE: December 16, 1997

PRIOR PRILOR APPLICATION NUMBER: 60/069, 870
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; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-944-396-103
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
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APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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APPLICATION NUMBER: 60/069,873
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APPLICATION NUMBER: 60/068,017
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Grimaldi, Christopher
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APPLICANT: Botstein, David
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Goddard, Audrey
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Hillan, Kenneth
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Wood, William
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                                               PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR PELING DATE: March 3, 1999
PRIOR FILING DATE: Warch 3, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: NO. US20020133675Alember 30, 1999
PRIOR FILING DATE: NO. US20020133675Alember 30, 1999
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PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR RAPLICATION NUMBER: PCT/US99/30095
PRIOR RILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR RILING DATE: February 11, 2000
PRIOR PLLING DATE: February 11, 2000
PRIOR PLLING DATE: FEBRUARY 11, 2000
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PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR PLING DATE: March 2, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: UJy 28, 2000
PRIOR FLING DATE: UJy 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/32678
PRIOR PLING DATE: PEDFURDATE: PCT/USO0/32678
PRIOR PLING DATE: February 28, 2001
NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
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Filvaroff, Ellen
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Matches 27; Conservative
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APPLICANT: Botstein, David
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US-09-944-432-103/c
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LENGTH: 27
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/943,762
CURRENT FILING DATE: 2001-09-26
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR PELING DATE: DECEMBER 3, 1997
PRIOR PELING DATE: DECEMBER 11, 1997
PRIOR FILING DATE: DECEMBER 11, 1997
PRIOR PELING DATE: DECEMBER 12, 1997
PRIOR PELING DATE: DECEMBER 12, 1997
PRIOR PELING DATE: DECEMBER 12, 1997
PRIOR PELING DATE: DECEMBER 16, 1997
PRIOR PELING DATE: DECEMBER 16, 1997
PRIOR PELING DATE: DECEMBER 16, 1997
PRIOR APPLICATION NUMBER: 60,069,696
PRIOR APPLICATION NUMBER: 60,069,694
                      PRIOR FILING DATE: February 22, 2000
PRIOR PLING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR PLING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR FILING DATE: December: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR PRILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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Patent No. US20020142958A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Kljavin, Ivar
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Goddard, Audrey
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Roy, Margaret
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Best Local Similarity
Matches 27; Conservat
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                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: PZ448P1C1.

CURRENT APPLICATION NUMBER: US/09/944,432

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-05-25

PRIOR PELICATION NUMBER: 60/067,411

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR FILING DATE: December 11, 1997
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FILING DATE: No. US20020142419Alember 30, 1999
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
FILING DATE: September 16, 1998
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APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
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R APPLICATION NUMBER: 60/069,278
R FILING DATE: December 11, 1997
R APPLICATION NUMBER: 60/069,425
R FILING DATE: December 12, 1997
R APPLICATION NUMBER: 60/069,696
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APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
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TITING DATE: December 17, 1997
TITING DATE: December 17, 1997
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APPLICATION NUMBER: 60/070,440
FILING DATE: January 5, 1998
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APPLICATION UNDBER: 60/074,092
FELING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
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APPLICATION NUMBER: 60/074,086
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APPLICATION UNDBER: 60/112, 850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113, 296
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APPLICATION NUMBER: 09/254,311
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Hillan, Kenneth
                                                                  Roy, Margaret
Tumas, Daniel
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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CURRENT PELLING DATE: 2001-09-26
PRIOR PULLING DATE: 2001-09-26
PRIOR PILLING DATE: 2001-05-25
PRIOR PILLING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/06/411
PRIOR APPLICATION NUMBER: 60/06/335
PRIOR PLILING DATE: December 11, 1997
PRIOR PILLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR PILLING DATE: December 16, 1997
PRIOR PILLING DATE: December 16, 1997
PRIOR PILLING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILLING DATE: December 16, 1997
PRIOR PILLING DATE: December 16, 1997
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APPLICATION NUMBER: PCT/US98/25108
                     1714 TGGGAAGATGGGCTTCAATTAGATGGC 1740
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RR APPLICATION NUMBER: 60/112,850
RR FILING DATE: December 16, 1998
RR APPLICATION NUMBER: 60/113,296
RR FILING DATE: December 22, 1998
RR APPLICATION NUMBER: 60/146,222
RR APPLICATION NUMBER: 60/146,222
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APPLICATION NUMBER: 60/070,440
FILING DATE: January 5, 1998
PAPPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
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PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
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                                                                                                                                                                                                                           Sequence 103, Application US/09944654
Patent No. US20020142959A1
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Hillan, Kenneth
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US-09-944-654-103/c
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                                                               PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR PILING DATE: December 18, 1997
PRIOR PILING DATE: December 19, 1997
PRIOR PILING DATE: December 19, 1998
PRIOR PILING DATE: December 19, 1998
PRIOR PILING DATE: Pebruary 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/071,986
PRIOR PILING DATE: Pebruary 9, 1998
PRIOR PILING DATE: Pebruary 9, 1998
PRIOR PILING DATE: Pebruary 25, 1998
PRIOR PILING DATE: Pebruary 26, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218.517
PRIOR PILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218.517
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 17, 1999
PRIOR PILING DATE: December 17, 1999
PRIOR PILING DATE: PEDFURATION NUMBER: PCT/US99/3009
PRIOR PILING DATE: PADFUCATION NUMBER: PCT/U
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
                           APPLICATION NUMBER: 60/069,
                                                         FILING DATE: December 16,
December 16,
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Best Local Similarity
Matches 27; Conserv
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Gaps

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27; Conservative

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PRIOR FILING DATE: December 1, 1998

PRIOR PILING DATE: December 16, 1998

PRIOR PELLON NUMBER: 09216, 517

PRIOR PELLON NUMBER: 09216, 517

PRIOR PELLON NUMBER: 09216, 517

PRIOR PELLON NUMBER: 0921, 1999

PRIOR PELLON NUMBER: POT/1999/28313

PRIOR PELLON NUMBER: POT/1999/283136

PRIOR PELLON NUMBER: POT/1999/28363136

PRIOR PELLON NUMBER: POT/1999/28363

PRIOR PELLON NUMBER: POT/1999/2836336

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Search completed: December 29, 2002, 02:21:45 Job time: 150 secs

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0149728-A 25 12-JUL-2001;
inc. (JP) ; SAGAMI CHEMICAL RESBARCH CENTER
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                                                             /note="unnamed protein product"
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Pred. No. 0;
                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
         Inc. (JP) ; SAGAMI
Location/Qualifiers
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                                     CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC
                                              CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC
                                                                                  GTCTGTGACATCGGCTACGGGGGGGGCCCAGTGTGCCCACCAAGGTGCATTTTCCCTTCCAC
                                                                                                                       TGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCCAGGGTCCTGAGGCCTGACCACA
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SQ Sequence 446 AA;

Ĥ 241 RINISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEGSCVCDIGYGGAQCATKVHFPFH 300 241 RINISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEGCSCVCDIGYGGAQCATKVHFPFH 300 121 VEVVSLWFAEGORYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180 61 WYOPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNWQLLPAGLASF 120 1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60 Gaps 96.8%; Score 2447.5; DB 22; Length 446; 97.1%; Pred. No. 2.4e-177; tive 1; Mismatches 3; Indels 9; Query Match 5.8. 96.8 Best Local Similarity 97.1 Matches 442; Conservative δλ g D OY à g

421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455

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PRO347; UNQ306; cancer; tumour; diagnosis; therapy; human; ss.
                                            CDNA clone encoding human PRO347, amplified in tumour cells.
                                                                                     Location/Qualifiers
123..1490
/*tag= a
123..200
/*tag= b
201..1487
/*tag= c
         AAX87260 standard; cDNA; 1876 BP.
                                                                                                                                                                                  98US-0109304.
98US-0070440.
98US-0083500.
98US-0086414.
                                                                                                                                                                     99WO-US00106.
                                    27-SEP-1999 (first entry)
                                                                                                                                            W09935170-A2.
                                                                                                                                                                                    20-NOV-1998;
05-JAN-1998;
29-APR-1998;
22-MAY-1998;
                                                                              Homo sapiens.
                                                                                                                                                                       05-JAN-1999;
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                                                                                                           sig_peptide
                                                                                                                        mat_peptide
                        AAX87260;
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This is the nucleotide sequence of cDNA clone DNA44176 (ATCC 209532) coding for human PRO347 (UNQ306) (see AAY06482). The clone was isolated from a foetal kidney library. Amplification of DNA44176 occurs in various tumours, suggesting an association with tumour formation or growth. Antagonists (e.g. antibodies) directed against PRO347 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour overexpression of the gene product and to contribute to tumour discoverexpression of the gene product and to contribute to tumour discoverexpression of the gene product and to contribute to tumour approach for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of
                                                                                                                                                                                                      Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment
                                                                                                Lawrence DA;
                                                                                              Hillan KJ,
                                                                                            Gurney AL,
                                                                                                                                                                                                                                                          Example 1; Fig 13; 162pp; English
 98US-0088742.
98US-0107783.
                                                                                          Goddard A,
                                                      (GETH ) GENENTECH INC
                                                                                                                                              1999-430385/36
                                                                                        Botstein D, Godd
Roy MA, Wood WI;
                                                                                                                                                                  P-PSDB; AAY06483
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10-JUN-1998;
10-NOV-1998;
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Sequence 1876 BP; 387 A; 568 C; 574 G; 347 T; 0 other;

240 AGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCCAACAGAC 120 GCTGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGACAGACCTGGCCC 360 CCGGAGCCCTGAACAGGAAGGAGTTTCTTGCTCCTCCCTGCACAACCGCCTGCGCA 300 AACTGGCTCAAGCCAGGGCAGCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCC 420 540 421 TOTGGCGCACCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCGGGGGGTTGGCGTCCT 480 480 481 TICITGAAGIGGICAGCCIAIGGITIGCAGAGGGGCAAGCGGIACAGCCACGCGGCAGGAG 540 541 AGTGTGCTCGCAACGCCACCTGCACCACTACACGCAGGTCGTGTGGGGCCACCTCAAGCC 600 0; Gaps CCATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGATCTCCTGGCTGTGCTCCTGGCCC TCCTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGG DB 20; Length 1876; Indels ; 0 100.0%; Sco... 100.0%; Pred. No. v. Best Local Similarity 100. Matches 1876; Conservative Query Match 61 361 121 181 241 241 301 301 qq ð g ŏ qq δý 엄 δŏ QQ oγ g δŏ δ δ

601 AGCTGGGCTGTGGGCGCACCTGGGCACCTGGGCAAACCGATAGACCCTTTGCTC 660 602 AGCTGGGCTGTGGGCGCACCTGGGCCACACCCACACCGATAGACCTTTGCTC 660 603 AGCTGGGCTGTGGGCGCACCTGGGCTCACGCCACACCGATACAA 700 604 GTGCCTCCCCCCGCACCACCTGGTCACCCCCACACCCTTTGCTC 670 605 GTGCCTCCCCCCCGCACACCTGGCTCACCCCCACACCCTTTGCTC 670 606 GTGCCTCCTCCCCCCCCCCACACCTGGTCACCCCCACACCCTTTGCTC 670 607 GTGCCTCCTCCCCCCCCCCCACCCCTGGTCTCACCCCTCTCACCCTCTCTC 670 607 GTGCCTCTCCTCTCTCTCCCCCCCACCCTGGTCTCTCACCCTCTCTCCTCTC 670 607 GTGCACCTGGTCTCTCTCTCCCCCCACACCCTTG 670 607 GTGCACCTGGTCTTCTCTCTCCCCCCACACCTTTGTCCCCATACCTTCTC 670 607 GTGCACCTGGTCTTTTCCCTCTCCCCCACACCTTTGTCCCCATACCTTTTCCCCTCTTTG 670 607 GTGCACCTGGTGTTTCCTCTTTTCCCCTTTTTTTCCTTTTTTCCTTTTTT	qa	541	
61 ARCTROGECTORGECACATCTCCCTTCCACACACCACACACCATTGTCTCCCCTATACA TO	δŏ 1	601	GCTGGGCTGTGGGCGCCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCT 66
10	q Q	601	CIGGGCIGIGGGCGCCACCIGIGCICIGCAGGCCAGCAGAGAAAAAAAA
721 AGGSTGCCTGGTGTTCGCTCGCACAGCCAGTGTTCAAAGCCTGGACC 760 721 AGGSTGCCTGGTGTTCGCTCTCCACACACCTGGACC 760 722 AGGSTGCCTGTGTGACGTCTCCACACACTGTCTCAAAGCCTGGACC 760 73 ATGCAGGGGGGTCTTGTGACGTCCCTCACACATGTCTCAAAGCTGCCACATG 810 74 TACCAGGGGGGGTCTTGTGACGTCCCACAGAATCT 910 75 ATGCAGGGGGGGTCTTGTGACGTCCCCAGAATCT 910 76 ATGCAGGGGGGGTCTTGTAACACTCCCACAGATCT 910 76 ATGCAGGGGGGCTCTTGAACACTCCCACAGATCT 910 76 ATGCAGGGGGGCTCTTGAACACTCCCACAGATCT 910 76 ATGCAGGGGGGCTCTTGAACACTCCCACAGATCT 910 76 ATGCAGTGAACATCACACACTCCCACAGATCTTCCCCTGGCTAACACGGGCAATACT 910 76 ATGCAGTGAACATCACACACTCCCACATGTCCACAGGTCCACACAGGTCCTTCCT	Qy Dp	661	SCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGA 72
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841 GACGTCTCAACATCAGCACTGCCACTGCCCCTGGCTACACGGCCACATACT 900 841 GACGTCTCAACATCACCACTGCCCACTGCCCCTGGCTACACGGCCACATACT 900 842 GACGTCTCAACACACACCTGCCCACTGCCCCTGCTTCTTTTTTTT	Ā G G	20 20	VECASGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCCCATGAGCTGCCAGAACCATG 84
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901 GCCAAGTGGAGGTGCAGGTGTGGAGGCGGGTTCGGGGGGGG	OD .	4	
901 GCGTCTGTGACATGGGGACCCGGGACGCGGACGGACGGAC	δλ	0	CCAAGTGAGGTGCAGCTGCAGTGTGTGCACGCCGGTTCCGGGAGGAGAGGAGTGCTCGT 96
961 QCGTCTGTGACATCGGCTACGGGGGACCCAGTGTGCCACCAGGTGCATTTTCCCTTCC 102 961 GCGTCTGTGACATCGGCTACGGGGGACCCAGTGTGCCACCAGGTGCATTTTCCCTTCC 102 961 GCGTCTGTGACCTGGGCTACGGGGGACCCCAGTGTGCCACCAGGTGCATTTTCCCTTCC 102 1021 ACACCTGTGACCTGACGGACACGGCACCATCATGTTCTTCAGGGCAGACACCT 108 1081 ATACAGGCAGGATCGACGGGACACTGCTTCATGTGTGTTCTTCAGGGCAGACACCT 104 1081 ATACAGGCAGGATCAGAGGACACGCTTCATGTGTGTTCTTCAGAGGCAGACACT 104 1081 ATACAGAGCAGGATCAAAGTGAGAGAACGGGGGTGCTGGCCCAGATCAAGACCC 114 1081 ATACAGAGCAGGATCAAAGTGAGAGAACGGGGGTGCTGGCCCAGATCAAGACCC 114 1081 ATACAGAGCAGGATCAAAGTGAGAGAAGCGGGGTGCTGGCCCAAACACAGAGCTA 120 1141 AGAAAGTGCAGGACATCAACAGGAAAGCGGGGTGCTGGCCCAAACACAACACAACACAACACAACACAACAACAAC	qq	901	CCAAGTGAGGTGCAGCCTGCAGTGTGCACGGCCGGTTCCGGGAGGAGGAGGACCTGCTGGT 96
991 GCGTCTGTGACATCGGCGAGCCCAGTGTGCCCACAGGTGCATTTTCCCTTCC	QY	9	CGTCTGTGACATCGGCTACGGGGGGGGGCCCAGTGTGCCACGAGGTGCATTTTCCCTTCC 10
1021 ACACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCACACCT 108	an	9	CGTCTGTGACATCGGCTACGGGGGGGGCCCAGTGCCACCAAGGTGCATTTTCCCTTCC 10
1021 ACACCTGTGACGACACGACACCTCTTCATGGTGTCTTCAGACCACACACCTT 1081 ACACCTGTGACCTCAGGGACACCCTT 1081 ATTACAGACCCAGGATCACAGGACACACACGACACCCTT 1081 ATTACAGACCCAGGATCAAGACCC 1141	δŏ	02	CACCTGTGACCTGAGGATCGACGGGGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCT 10
1081 ATTACAGNGCCAGGATGAAATGTCAGAGGAAGGGGGGGTGCTGGCCCCAGATCAAGAGC 114	qq	1021	CACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTTTTCAGAGGCAGACACCT 10
1081 ATTACAGAGCCAGGATGAANTGTCAGAGGAANGGCGGGTGCTCAGAGGCC	Qy	08	ATGAAATGTCAGAGAAAGGCGGGGTGCTGGCCCCAGATCAAGAGCC 11
141 AGAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGCTGGAGCCACCAACGAGGTGA 120 1141 AGAAGTGCAGGACATCCTCGCCTTTTTTT	Op	1081	ATGAAATGTCAGAGGAAAGGCGGGGTGCTGGCCCAGATCAAGAGCC 11
1141 AGAAGTGCAGGACTTCTATCTGCCCCTGGAGCCACCACGAGGTGA 1201 CTGACAGTGCACCAGGAACTTCTGGATCGGCCCCTGGAGCCCCCCAGGGT26 1201 CTGACAGTGCTTCGAGCCAGGAACTTCTGGATCGGCTCACCTACAAGACCGCCAAGG 126	ΟŽ	14	TCCTCGCCTTCTATCTGGGCCGCCTGGAGACCACCAACGAGGTGA 12
1201 CTGACAGTGACTTCGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGG 126 12	qq	14	reducecciicialifice de concentral de la 12
1201 CTGACAGTGACTTCGAAACTTCTCTTTTTTTTTTTTTTT	οy	1201	TGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGG 12
1261 ACTCCTTCGGCTGGCCAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGCCAGC 132 1261	qa	1201	TGACAGTGACTTCGAGAACCAGGAACTTCTGGATCGGGCTCACCTACAAGACCGCCAAGG 12
1261 ACTCCTTCCGCTGGGCCACAGGGGAGCCTCTCTCTTTTTTTT	QY	1261	CTCCTTCGGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTTGGGCAGC 13
1321 CTGACAACCACGGGCTGGTGTGCCATGGGGTTTGGCAACTGCGTGGAGC 138	qq	~	TICTICGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTGCCTTTGGGCAGC 13
1321 CTGACACCACGGGCTGGTGTGTTTTTTTTTTTTTTTTTT	QY	1321	SACAACCACGGGTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGC 13
1381 TGCAGGCTTCAGCTGCAACGACGACGCGCAAAACCGGAAACCGTTACA 144	DÞ	32	SACAACCACGGGCTGGTGTGTGTGTGTGCTGCCATGGGGTTTGGCAACTGCGTGGGAGC 13
1381 TCCAGGCTTCAGCTGCAGCTGCAGCTGCAAACCCGGAACCGTTACA 144 1441 TCTGCCAGTTTGCCCGGAGCCACCGGGGGCCCGGGGCCCGGAACCCTTACA 150 1441 TCTGCCAGTTTGCCCGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCGTACA 150 1501 CATGCCAGTTTGCCCTGGAGCACATCTCCCGGTGGGCCCAGGGTCCTGAGGCCTGACA 150 1501 CATGCCAGTTTGCCCTGGAGCACATCTCCCGGTCCTACCTGCTCTGCCCACCTGT 156 1501 CATGGCTCCCTGCCTGGGAGCACGGCTCTGCTTACCTGTCTGCCCACCTGT 156 1501 CATGGCTCCTGCCTGGGAGCACGGCTCTGCTTACCTGTCTGCCCACCTGTC 156 151	0	38.	LAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACA 14
1441 TCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCA 150	QQ	1381	CAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACGGTTACA
1441 TCTGCCAGTTTGCCCAGGAGCATCTCCCGGTGGGGCCCAGGGTCCTGAGGCTCTGTGTTTTTTTT	ď.	1441	CTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCCAGGGTCCTGAGGCCTGACCA 15
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1561 GGAACAAGGGCCAGGTTAAGACCACACGCTCATHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Οy	56	SAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCAC 16
1621 AATGCCAGAAGTTGGGCAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGAGT	đ	. 26	GAACAAGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTTTCAGACGTTGTCACA 16
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_	1621 AATGCCAGAAGTTGGGCAGAGAGAAGCAGGGAGGCCAGTGAGGGCCAGGGAGTGAGT	1680
-	1681 AGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740	1740
₽	1681 AGAAGAAGCTGGGGCCCTTCGCCTGCTTTGATTGGGAAGATGGGCTTCAATTAGATGGC 1740	1740
-	1741 GAAGGAGAGACCACCAGTGGTCCAAAAAGGCTGCTCTTCCACCTGGCCCAGACCC 1800	1800
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1801	TGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAATCAG 1860	1860
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            187 CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGGTGCAGGAGCAGGTTGGCC 246
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                            Library was constructed by Dr. Manfred Gessler.
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//lab host prepared from a pool of 6 anonymous Wilms' tumor RMAs.

Ras prepared from a pool of 6 anonymous Wilms' tumor RMAs.

//lab BRL/Life Tech. CDNA library preparation was with

//lab BRL/Life Tech. Superscript Plasmid system. An

Oligo-dT Wotl primer for first strand synthesis generated

gdgpcogccc(t)n at the 3' end of the clones. A S. Sail

Oligo-dT Wotl primer for first strand synthesis generated

adaptor was used with sequence 5'-gtogaccagoggtcog-3'.

Salphort was used with sequence 5'-gtogaccagoggtcog-3'.

Salphort was used with sequence 5'-gtogaccagoggtcog-3'.

Library was constructed by Dr. Manfred Gessler."
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                                                                                          \cjous="IMAGE:1700537"
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Seq primer: -40RP from Gibco
        Lyis 2, resednenced clone was no breatons 2, data to verify this information
    This clone is swallable royalty-free through LLNL; contact the This clone is swallable royalty-free through LLNL; contact through the further information. This read is a RESEQUENCE of a previously sequenced human clone original clone citation: see original entry for original citation original clone citation.
                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
                                                                                                                                                                                    COMMENT
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                                                                                                                                                                               JOURNAL
    MCI/MIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
McI/MIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Mational Cancer Institute / Wational Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; J. (bases 1 to 463)
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                    SU34D09.75 Gessler Wilms tumor Homo saptens cDNA clone
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mRNA linear EST 02-JUL-1999
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emstr-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                              tb28dll.x1 NCI_CGAP_Kidl2 homo sapiens cDNA clone IMAGE:2055669 3' similar to TR:Q61830 Q61830 MANNOSE RECEPTOR, C TYPE 1 PRECURSOR ;, AI307814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Kidney; Vector: p1713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction, by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 617)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Insert Length: 725 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
Location/Qualifiers
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KEYWORDS
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27.3%; Score 512; DB 9; Length 617; 100.0%; Pred. No. 1.8e-161; tive 0; Mismatches 0; Indels

Conservative

512;

Matches

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RESULT 11
       AAZ23300
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AAZ23300 standard; cDNA; 1338 BP

AAZ23300;

31-JAN-2000 (first entry)

Human T139 protein coding sequence.

Human; T139 polypeptide; immune system disorder; spermatogenesis; ss; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping

Homo sapiens.

W09954343-AZ:

28-OCT-1999

23-APR-1999; 99WO-US08896.

98US-0065661 23-APR-1998; (MILL-) MILLENNIUM BIOTHERAPEUTICS INC

Holtzman D;

WPI; 1999-633969/54. P-PSDB; AAY41266.

Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression or activity

Claim 2; Page 114; 115pp; English.

This represents the coding sequence of the human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 cDNA insert is deposited with AprC under accession number of the T139 polypeptides and polynucleotides can be administered 98644. The T139 polypeptides and polynucleotides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant T139 expression or activity, especially proliferative or differentiative disorders, e.g. as a contraceptive to decrease sociated modulate spermatogenesis, e.g. as a contraceptive to decrease contractogenesis or to treat disorders related to defects in sperm-egg fusion. They may also be useful to treat testicular disorders e.g. testicular cancer. The polypeptides may be used to identify selectively binding compounds which may be useful for detecting the polypeptide activity. The polynucleotides medulating polypeptide activity. The selectively hybridize to the polynucleotides which may be useful for detecting the polynucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant T139 levels; determining if a gene calls or tissues expressing aberrant T139 levels; determining if a gene calls or tissues expressing aberrant T139 levels; determining if a gene calls or tissued with T139 expression a activity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate/prevent T139 expression.

Sequence 1338 BP; 259 A; 420 C; 413 G; 246 T; 0 other;

Ξ, 123 AIGCIGCAICCAGAGACCICCCTGGCCGGGGGCAICICCTGGCIGTGCICCIGGCCCIC 182 242 TGGGTCCAGCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA 362 Ouery Match .68.9%; Score 1293; DB 20; Length 1338; Best Local Similarity 97.7%; Pred. No. 5.2e-301; Matches 1333; Conservative 0; Mismatches 5; Indels 27; Gaps 183 CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC Query Match 61 303 181 363 δ g q ŏ g ò a

241

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This represents a human T139 polypeptide. The T139 polypeptide can be expressed by standard recombinant methodology. The T139 cDNA insert is deposited with ATCC under accession number 98694. The T139 polypeptides can be administered therapeutically or prophylactically to treat/prevent disorders associated with aberrant T139 cprphylactically to treat/prevent disorders associated with aberrant T139 cprphylactically to treat/prevent disorders associated with aberrant T139 cprpression or activity, especially proliferative or differentiative concerns e.g. of the immune system. They can be used to modulate concerns the spermatogenesis or concraceptive to decrease spermatogenesis or to treat disorders related to defects in sperme egg fusion. They may also compounds modulating polypeptides of the sectivity binding compounds which may be useful for detecting the polypeptides in samples; and identifying compounds modulating polypeptide activity. The polynucleotides are useful cor producing probes or primers that selectively hybridize to the compounds which may be useful for detecting the polymucleotides in a sample, gene mapping; identifying cells or tissues expressing aberrant concerns and providers and the may be useful for detecting the polymucleotides in asmple, gene mapping; identifying cells or tissues expressing aberrant concerns and providers at risk for or having a disorder associated with T139 chockers or a certifity and to monitor therapeutic interventions; and for producing antisense sequences for therapeutic administration to modulate Human: T139 polypeptide; immune system disorder; spermatogenesis; sperm-egg fusion; testicular disorder; testicular cancer; gene mapping. Human T139 nucleic acids and polypeptides, useful for treating proliferative disorders associated with aberrant T139 expression or activity (MILL-) MILLENNIUM BIOTHERAPEUTICS INC. AAY41266 standard; Protein; 446 AA Claim 9; Fig 1; 115pp; English. 96880SD-0M66 98US-0065661 WPI; 1999-633969/54. N-PSDB; AAZ23299, AAZ23300. 31-JAN-2000 (first entry) Human T139 protein. W09954343-A2. 23-APR-1998; Homo sapiens 23-APR-1999; 28-OCT-1999 Holtzman D; AAY41266; RESULT 4
AAY41266

Sequence 446 AA;

Query Match 96.8%; Score 2447.5; DB 20; Length 446; Best Local Similarity 97.1%; Pred. No. 2.4e-177; Matches 442; Conservative 1; Mismatches 3; Indels 9; Gaps

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OY 1 MLHPETSPGRGHLLAVLIALLGTIWAĒVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60 1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPWAGALNRKESFLLLSLHNRLRS 60

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qq	241	RINISTCHCHOPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH	30
à	301	TODLRIDGDCFMYSSEADTYTRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT	36
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Dp	301	TCDLRIDGDCFMVSSEADTYTRARMKCQRKGGVLAQIKSQKVQDILAFILGKLEIINEVI	2
QY	361	DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL	42
QQ	361		41
οy	421	QASAAFNWNDQRCKTRNRYICOFAQEHISRWGPGS 455	
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661 TCCTTNCCCTGGGCCACGGGGACCACAG 690
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LOCATION: (i)...(690)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 321
                                                                                                  APPLICANT: Michamarinova

APPLICANT: Micham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TILLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

TILLE OF INVENTION: 10121,462C2

CURRENT FILING DATE: 1999-09-24

CURRENT FILING DATE: 393

SOFTWARE: Facter of Windows Version 3.0

SOFTWARE: Facter for Windows Version 3.0
                                      COMPOSITIONS AND METHODS FOR THE THERAPY AND
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                            Sequence 321, Application US/09404879A Patent No. 6468546
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1257. 4398,4873. 5060,5577. 5718,6208. 6489)
/gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 7215)
Fernandez-Salguero, P., Hoffman, S.M., Cholerton, S., Mohrenweiser, H., Raunio, H., Rautio, A., Pelkonen, O., Huang, J.D., Evans, W.E., Idle, J.R. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A genetic polymorphism in coumarin 7-hydroxylation: sequence of the human CYP2A genes and identification of variant CYP2A6 alleles Am. J. Hum. Genet. 57 (3), 651-660 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAB40518.1"
/db.xref="G1:1008462"
/db.xref="G1:100846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSTHGANIDPTFELSRIVSNYISSIVFGDRFDYKDKEFLSLLRMALGIFQFTSTSTGQ
LYEMFSSVMKHLPGPQQQAFQLLQGLEDFIAKKVEHNQFTLDPNSPRDFIDSFLIRMQ
EEEKNPNTEFYLKNLMMSTLNLFIAGTETVSTTLHYGFLLLMKHPEVEAKVHEEIDRV
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PMLGSVLRDLRFPSNPRDFNPQHFLGEKGOFKKRDAFVPFSIRKRNCFGEGLARMELF
LFFTTVMONFRLKSSQSPKDIDVSPKHVGFATIPRNYTWSFLPR"
                                                             PRI 01-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 7215)
Fernandez-Salguero, P.
Direct Submission
Direct Submission
Institutes (01-MAR-1995) Pedro Fernandez-Salguero, National
Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20894, USA
Location/Qualifiers
1. 7215
/organism="Homo sapiens"
/db_xref_"taxon:9606"
                                           HSU22U27 7215 bp DNA linear F
Human cytochrome P450 (CYP2A6V2) gene, complete cds.
U22027
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6308. .6489 , ,
/gene="CYP2A672"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499. .2659
gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1237. .1399
/gene="CYP2A6V2"
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'gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4257. .4398
/gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4873. .5060
/gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5577. .5718
/gene="CYP2A6V2"
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/gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1207. .3383
'gene="CYP2A6V2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90. .6744
2196 c
                                                                                                                                                                           U22027.1 GI:1008461
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ORIGIN

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Query Match
Best Local Similarity 100.0%; Pred. No. 7.4; **
Matches 21; Conservative 0; Mismatches; '0; Indels 0; Gaps 0;
Qy 1634 GGCAGAGAGAGAGGCAGGAGG 1654
Db 1605 GGCAGAGAGGCAGGAGG 1585
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